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SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

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STAFF USE ONLY

Date completed: 08-20-02
Searcher: Beverly C4994
Terminal time: 20
Elapsed time: _____
CPU time: _____
Total time: 25
Number of Searches: _____
Number of Databases: 1

Search Site

_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
☒ Other CGN

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 19:24:00 ; Search time 1864.41 Seconds
(without alignments)
8350.815 Million cell updates/sec

Title: US-09-898-554-13

Perfect score: 744
Sequence: 1 atgaccttgcagcaagat.....caatcattgcaattg 744

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenBankl:
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_ph:*
7: gb_pl:*
8: gb_pr:*
9: gb_ro:*
10: gb_ro:*
11: gb_ro:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_ph:*
24: em_pl:*
25: em_pl:*
26: em_ro:*
27: em_ro:*
28: em_ro:*
29: em_vl:*
30: em_vl:*
31: em_vl:*
32: em_vl:*
33: em_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Score Match Length DB ID Description

1	668.2	89.8	3763	10	AF303744	AF303744 Mus muscu
2	526.8	70.8	3750	10	AB005900	AB005900 Rattus no
3	298.2	40.1	1318	6	AR077718	AR077718 Sequence
4	298.2	40.1	1318	6	AR138263	AR138263 Sequence
5	298.2	40.1	1318	6	E12916	E12916 Human CDNA
6	298.2	40.1	2067	9	AF035776	AF035776 Homo sapi
7	298.2	40.1	2463	9	AB010710	AB010710 Homo sapi
8	298.2	40.1	2480	9	BC022295	BC022295 Homo sapi
9	293.6	39.5	1578	4	AB018668	AB018668 Sus scrof
10	287.2	38.6	1879	4	D89049	D89049 Bos taurus
11	287.2	38.6	1897	6	AR077716	AR077716 Sequence
12	287.2	38.6	1897	6	AR138261	AR138261 Sequence
13	287.2	38.6	1897	6	E12914	E12914 Bovine CDNA
14	287.2	38.6	1906	6	AR077717	AR077717 Sequence
15	287.2	38.6	1906	6	AR138262	AR138262 Sequence
16	287.2	38.6	1906	6	E12915	E12915 Bovine CDNA
17	277.6	37.3	1514	4	AB016237	AB016237 Oryctolag
18	127.8	17.2	278	10	AB01809753	AB01809753 Rattus no
19	125.4	16.9	162	10	AB01809755	AB01809755 Rattus no
20	114.4	15.4	161	10	AB01809756	AB01809756 Rattus no
21	108.4	14.6	169	10	AB01809758	AB01809758 Rattus no
22	106.2	14.3	162	10	AB01809754	AB01809754 Rattus no
23	103	13.8	240864	2	AC006510	AC006510 Homo sapi
24	102	13.7	260	9	AB017441	AB017441 Homo sapi
25	102	13.7	328	9	HS0183	HS0183 Homo sapi
26	102	13.7	15387	9	HS01831757	HS01831757 Homo sapi
27	102	13.7	182211	2	AC024224	AC024224 Homo sapi
28	90.6	12.2	140	10	AB01809757	AB01809757 Rattus no
29	74.4	10.0	534	6	E21012	E21012 Novel membr
30	74.4	10.0	741	6	E21012	E21012 Novel membr
31	74.4	10.0	744	9	AY026769	AY026769 Homo sapi
32	74.4	10.0	744	9	AF400595	AF400595 Homo sapi
33	74.4	10.0	1153	9	HS01831757	HS01831757 Homo sapi
34	74.4	10.0	1606	9	AF313468	AF313468 Homo sapi
35	74.4	10.0	2681	9	HS01831757	HS01831757 Homo sapi
36	74.4	10.0	240864	2	AC006510	AC006510 Homo sapi
37	73.4	9.9	154	9	AB017442	AB017442 Homo sapi
38	72.4	9.7	507	9	AF400599	AF400599 Homo sapi
39	72.4	9.7	603	6	E21011	E21011 Novel membr
40	72.4	9.7	606	9	AY026770	AY026770 Homo sapi
41	72.4	9.7	606	9	AF400596	AF400596 Homo sapi
42	72.4	9.7	990	6	AR035946	AR035946 Sequence
43	72.4	9.7	990	6	AR080819	AR080819 Sequence
44	72.4	9.7	1015	9	HS01831757	HS01831757 Homo sapi
45	72.4	9.7	2349	9	AF313469	AF313469 Homo sapi

ALIGNMENTS

RESULT 1
AF303744 AF303744 3763 bp mRNA ROD 02-JAN-2001
LOCUS Mus musculus oxidized LDL receptor (Lox-1) mRNA, complete cds.
DEFINITION AF303744
ACCESSION AF303744
VERSION AF303744.1 GI:12006985
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus.

REFERENCE
1 (bases 1 to 3763)
Mammalia: Eutheria; Rodentia: Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Park,S.-H., Ahn,H.-J. and Cho,J.-J.
TITLE Mouse Lox-1 is expressed in mast cells after Ige cross-linking
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3763)
Park,S.-H., Ahn,H.-J. and Cho,J.-J.
AUTHORS Direct Submission
TITLE Submitted (07-SEP-2000) Microbiology, Kyung Hee University, College
JOURNAL of Medicine, Dongdaemun-Gu, Hocki-Dong 1, Seoul, Korea
FEATURES
source 1..3763
/organism="Mus musculus"

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OK protein - protein search, using sw model

Run on: August 19, 2002, 22:57:24 ; Search time 68.99 Seconds

(without alignments)
619.361 Million cell updates/sec

Title: US-09-898-554-14

Perfect score: 1339

Sequence: 1 MTFDDKMKPANDEPDQKSCG.....ENCILIAFSICCKTKNHLQI 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMBL_19:
2: sp_archaea:
3: sp_bacteria:
4: sp_fungi:
5: sp_human:
6: sp_invertebrate:
7: sp_mammal:
8: sp_mhc:
9: sp_organellar:
10: sp_phage:
11: sp_plant:
12: sp_rodent:
13: sp_virus:
14: sp_vertebrate:
15: sp_unclassified:
16: sp_virus:
17: sp_bacteriap:
18: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1241	94.1	363	11	09EQ09
2	972	73.7	364	11	070156
3	643	48.7	278	6	09XTRA8
4	639	48.4	274	6	09TWR7
5	637	48.3	273	4	P78380
6	596	45.2	270	6	P79391
7	258	19.6	247	4	09BXN2
8	251.5	19.1	168	4	096PA7
9	251	19.0	201	4	09HAK3
10	231	17.5	244	11	09J150
11	224.5	17.0	381	6	095LA8
12	223.5	16.9	381	6	095LC6
13	223	16.9	360	4	096Q04
14	223	16.9	380	4	096Q05
15	223	16.9	380	4	096Q00
16	223	16.9	404	4	09NNX6

17	223	16.9	404	4	096Q01	096q01 homo sapien
18	222.5	16.9	404	6	095J96	095j96 macaca mla
19	221	16.8	280	4	09NZH3	09nzh3 homo sapien
20	219.5	16.6	223	11	0925G3	0925g3 mus musculu
21	218.5	16.6	217	11	0642Z8	0642z8 mus sp. nk1
22	216.5	16.4	275	11	09D403	09d403 mus musculu
23	212	16.1	268	4	096Q03	096q03 homo sapien
24	212	16.1	404	6	095I98	095i98 pan troglod
25	211	16.0	334	4	096Q09	096q09 homo sapien
26	210	15.9	334	4	096Q08	096q08 homo sapien
27	206.5	15.7	398	4	0925G4	0925g4 mus musculu
28	205	15.5	312	4	096Q07	096q07 mus musculu
29	204.5	15.5	223	11	099JB4	099jb4 mus musculu
30	204.5	15.5	223	11	099P32	099p32 mus musculu
31	203.5	15.4	295	11	0912M4	0912m4 mus musculu
32	203.5	15.4	311	11	098SV4	098sv4 mus musculu
33	203.5	15.4	325	11	0912X9	0912x9 mus musculu
34	202.5	15.4	227	11	061973	061973 mus musculu
35	201.5	15.3	227	11	091V25	091v25 mus musculu
36	200.5	15.2	223	11	0925G5	0925g5 mus musculu
37	195.5	14.8	224	11	061970	061970 mus musculu
38	192.5	14.6	189	11	061969	061969 mus musculu
39	192.5	14.6	263	4	096Q03	096q03 mus musculu
40	191.5	14.5	229	11	09JL99	09jl99 mus musculu
41	191	14.5	332	4	096Q05	096q05 mus musculu
42	190	14.4	309	11	063097	063097 mus musculu
43	189.5	14.4	198	11	09D8L1	09d8l1 mus musculu
44	187.5	14.2	156	13	073894	073894 gallus gall
45	186.5	14.1	230	11	054871	054871 rattus norv

ALIGNMENTS

RESULT 1.
ID 09EQ09 PRELIMINARY; PRT; 363 AA.
AC 09EQ09;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE OXIDIZED LDL RECEPTOR.
GN LOX-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Park S.-H., Ahn H.-J., Cho J.-J.;
RT "Mouse LOX-1 is expressed in mast cells after Ige cross-linking."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF303744; AAC4498.1; -
DR InterPro: IPR001304; lectin.C.
DR Pfam: PF00059; lectin.C; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PSS0041; C_TYPE_LECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 363 AA; 41613 MW; E44703D6408F15P8 CRC64;

Query Match 94.1%; Score 1241; DB 11; Length 363;
Best Local Similarity 67.5%; Pred. No. 4.6e-80;
Matches 245; Conservative 0; Mismatches 2; Indels 116; Gaps 1;

QY 1 MTFDDKMKPANDEPDQKSCGKKR-----24
DB 1 MTFDDKMKPANDEPDQKSCGKKRGLHLLSPWFPAAATLVILCVLSTLVQMTOLR 60
QY 25 -----24
DB 61 QVSDLKQYQANLTQDRILLEGQWLAQQAENASQESKELKGIPTLTOKLNEKSEOE 120

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OY 25 -----ESORELKGIDITITRKLDEKSEKEOELLQONLQEAQ 64
DB 121 ELLQKNQNLQEAQRAANSSESORELKIDITITRKLDEKSEKEOELLQONLQEAQ 180
OY 65 RAANSSESORELKIDITITRKLDEKSEKEOELLQONLQEAQRAANSFCPCQDWI 124
DB 181 RAANSSESORELKIDITITRKLDEKSEKEOELLQONLQEAQRAANSFCPCQDWI 240
OY 125 WKRENCYLPHGPFWEKKNQTCOSLGQOLQINGADDLFFIIQAIHSHTSPFWIGLHRRK 184
DB 241 WKRENCYLPHGPFWEKKNQTCOSLGQOLQINGADDLFFIIQAIHSHTSPFWIGLHRRK 300
OY 185 PGQPLWENGTPLNFOFFTRGVSLQIYSSNCAYLQDGAFAENCILIAFSICOKKTNH 244
DB 301 PGQPLWENGTPLNFOFFTRGVSLQIYSSNCAYLQDGAFAENCILIAFSICOKKTNH 360
OY 245 LQI 247
DB 361 LQI 363

RESULT 2
ID 070156 PRELIMINARY: PRT: 364 AA.
AC 070156:
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ENDOTHELIAL RECEPTOR FOR OXIDIZED LOW-DENSITY LIPOPROTEIN.
GN LOX-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SHR.SP.; TISSUE=KIDNEY;
RX MEDLINE=98181826; PubMed=9494115;
RA Nagase M., Hirose S., Fujita T.;
RT "Unique repetitive sequence and unexpected regulation of expression of
RT rat endothelial receptor for oxidized low-density lipoprotein (LOX-
RT 1).";
RL Biochem. J. 330:1417-1422(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
RX MEDLINE=99057940; PubMed=9837956;
RA Nagase M., Abe J., Takahashi K., Ando J., Hirose S., Fujita T.;
RT "Genomic organization and regulation of expression of the lectin-like
RT oxidized low-density lipoprotein receptor (LOX-1) gene.";
RL J. Biol. Chem. 273:33702-33707(1998).
DR EMBL; AB005900; BAA25785.1; -
DR EMBL; AB018104; BAA35123.1; -
DR EMBL; AB018097; BAA35123.1; JOINED.
DR EMBL; AB018098; BAA35123.1; JOINED.
DR EMBL; AB018099; BAA35123.1; JOINED.
DR EMBL; AB018100; BAA35123.1; JOINED.
DR EMBL; AB018101; BAA35123.1; JOINED.
DR EMBL; AB018102; BAA35123.1; JOINED.
DR EMBL; AB018103; BAA35123.1; JOINED.
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lipoprotein; Receptor; Lectin.
SQ SEQUENCE 364 AA; 41890 MW; 0AD2839C07206E09 CRC64;

Query Match 73.7%; Score 972; DB 11; Length 364;
Best Local Similarity 53.2%; Pred. No. 4.3e-61;
Matches 192; Conservative 23; Mismatches 30; Indels 116; Gaps 2;
1 MTFDDKMPANDEPDKSGKKPK----- 24

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DB 1 MAFDDKMKFVNGPDPDKSGKKPKGLHLSSWPCPAVTLATLCVLSVTLIVQOTOLL 60
OY 25 -----ESORELKGIDITITRKLDEKSEKEO 50
DB 61 QVSDLLKQYQANLTQODHILEGOMSAOKKAENASQSKRELKQIDITITRKLDEKSEKEO 120
OY 51 ELLQKNQNLQEAQRAANS----- 69
DB 121 KLLQKNQNLQEAQRAANSSESKMELKQIDITITRKLDEKSEKEOELLQONLQEAQ 180
OY 70 -----SESORELKIDITITRKLDEKSEKEOELLQONLQEAQRAANSFCPCQDWI 124
DB 181 KAKYSESORELKQIDITITRKLDEKSEKEOELLQONLQEAQRAANSFCPCQDWI 240
OY 125 WKRENCYLPHGPFWEKKNQTCOSLGQOLQINGADDLFFIIQAIHSHTSPFWIGLHRRK 184
DB 241 WKRENCYLPHGPFWEKKNQTCOSLGQOLQINGADDLFFIIQAIHSHTSPFWIGLHRRK 300
OY 185 PGQPLWENGTPLNFOFFTRGVSLQIYSSNCAYLQDGAFAENCILIAFSICOKKTNH 244
DB 301 PNHFWMENGSPISLFOFFTRGVSLQIYSSNCAYLQDGAFAENCILIAFSICOKKTNH 360
OY 245 L 245
DB 361 L 361

RESULT 3
ID 09XTA8 PRELIMINARY: PRT: 278 AA.
AC 09XTA8:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE LECTIN-LIKE OXIDIZED LDL RECEPTOR.
GN LOX-1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Sawamura T., Chen M.;
RT "Rabbit lectin-like oxidized LDL receptor 1.";
RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016237; BAA81912.1; -
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 278 AA; 31646 MW; 25A5E310F82A098 CRC64;

Query Match 48.7%; Score 643; DB 6; Length 278;
Best Local Similarity 49.3%; Pred. No. 5.1e-38;
Matches 135; Conservative 39; Mismatches 70; Indels 30; Gaps 6;
1 MTFDDKMPANDEPDKSGKKPK-----GKIDTTR--- 40
DB 5 MAVDDIKVPMKDPDKSGKKPK--GIRFTSPWPCPAVALGVLCGSLMTITLMGM 62
OY 41 ---KLDEKSEKEOELLQONLQEAQRAANSSESORELKIDITITRKLDEKSK 93
DB 63 QLLQVSDLLKQQAANTLTQDHTLEGGVTLQQAQEAASQSOSEKLEMITTLARLDEKSK 122
OY 94 EQEELLQKNQNLQEAQRAANSFCPCQDWIWKRENCYLPHGPFWEKKNQTCOSLGQOL 152
DB 123 KQELNHWYLVNLQEAQLKRDNFSGPCPELWGHKKNCYLFSSGSPFWESSQKCLSLNQ 182
OY 153 LLIQINGADDLFFIIQAIHSHTSPFWIGLHRRKPGQPLWENGTPLNFOFFTRGVSLQIY 212

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OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 19:24:00 : Search time 1864.41 Seconds

(Without alignments)
8550.815 Million cell updates/sec

Title: US-09-898-554-13

Perfect score: 744

Sequence: 1 atgacttttgatgcacaagat.....caatcattgcaatttag 744

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenBml : *

1: gb_ba : *

2: gb_htg : *

3: gb_in : *

4: gb_om : *

5: gb_ov : *

6: gb_pat : *

7: gb_ph : *

8: gb_pl : *

9: gb_pr : *

10: gb_ro : *

11: gb_sts : *

12: gb_sy : *

13: gb_un : *

14: gb_vi : *

15: em_ba : *

16: em_fun : *

17: em_hum : *

18: em_in : *

19: em_mu : *

20: em_om : *

21: em_or : *

22: em_ov : *

23: em_pat : *

24: em_ph : *

25: em_pl : *

26: em_ro : *

27: em_sts : *

28: em_un : *

29: em_vi : *

30: em_htg_hum : *

31: em_htg_inv : *

32: em_htg_other : *

33: em_htg_inv : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match Length	ID	Description
1	AF303744	3763	10	AF303744	Mus musculus oxidized LDL receptor (Lox-1) mRNA, complete cds.

1	658.2	89.8	3763	10	AF303744	AF303744 Mus muscu
2	526.8	70.8	3750	10	AB005900	AB005900 Rattus no
3	298.2	40.1	1318	6	AR077718	AR077718 Sequence
4	298.2	40.1	1318	6	AR138263	AR138263 Sequence
5	298.2	40.1	1318	6	E12916	E12916 Human cDNA
6	298.2	40.1	1318	6	AF035776	AF035776 Homo sapi
7	298.2	40.1	2463	9	AB010710	AB010710 Homo sapi
8	298.2	40.1	2480	9	BC022295	BC022295 Homo sapi
9	293.6	39.5	1578	4	AB018668	AB018668 Sus scrofa
10	287.2	38.6	1879	4	DB9049	DB9049 Bos taurus
11	287.2	38.6	1897	6	AR077716	AR077716 Sequence
12	287.2	38.6	1897	6	AR138261	AR138261 Sequence
13	287.2	38.6	1897	6	E12914	E12914 Bovine cDNA
14	287.2	38.6	1906	6	AR077717	AR077717 Sequence
15	287.2	38.6	1906	6	AR138262	AR138262 Sequence
16	287.2	38.6	1906	6	E12915	E12915 Bovine cDNA
17	277.6	37.3	1514	4	AB016237	AB016237 Oryctolag
18	127.8	17.2	270	10	AB018097S3	AB018097 Rattus no
19	125.4	16.9	162	10	AB018097S5	AB018097 Rattus no
20	114.4	15.4	161	10	AB018097S6	AB018097 Rattus no
21	108.4	14.6	169	10	AB018097S8	AB018097 Rattus no
22	106.2	14.3	162	10	AB018097S4	AB018097 Rattus no
23	103	13.8	240864	2	AC006510	AC006510 Homo sapi
24	102	13.7	260	9	AB017441	AB017441 Homo sapi
25	102	13.7	328	9	HSOLR3	AF079166 Homo sapi
26	102	13.7	15387	9	HSAL131757	AJ131757 Homo sapi
27	102	13.7	182211	2	AC024224	AC024224 Homo sapi
28	90.6	12.2	140	10	AB018097S7	AB018097 Rattus no
29	74.4	10.0	534	6	E21014	E21014 Novel membr
30	74.4	10.0	741	6	E21012	E21012 Novel membr
31	74.4	10.0	744	9	AY026769	AY026769 Homo sapi
32	74.4	10.0	744	9	AF400595	AF400595 Homo sapi
33	74.4	10.0	1153	9	HSAL132373	AJ132373 Homo sapi
34	74.4	10.0	1606	9	AF313468	AF313468 Homo sapi
35	74.4	10.0	2681	9	HSOLR4	AF079167 Homo sapi
36	74.4	10.0	240864	2	AC006510	AC006510 Homo sapi
37	73.4	9.9	154	9	AB017442	AB017442 Homo sapi
38	72.4	9.7	507	9	AF400599	AF400599 Homo sapi
39	72.4	9.7	603	6	E21011	E21011 Novel membr
40	72.4	9.7	606	9	AY026770	AY026770 Homo sapi
41	72.4	9.7	606	9	AF400596	AF400596 Homo sapi
42	72.4	9.7	990	6	AR035946	AR035946 Sequence
43	72.4	9.7	990	6	AR080819	AR080819 Sequence
44	72.4	9.7	1015	9	HSAL132372	AJ132372 Homo sapi
45	72.4	9.7	2349	9	AF313469	AF313469 Homo sapi

ALIGNMENTS

RESULT 1

AF303744 LOCUS AF303744 Mus musculus oxidized LDL receptor (Lox-1) mRNA, complete cds.

VERSION AF303744.1 GI:12006985

KEYWORDS

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 3763)

AUTHORS Park, S.-H., Ahn, H.-J. and Cho, J.-J.

TITLE Mouse Lox-1 is expressed in mast cells after Ige cross-linking

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 3763)

AUTHORS Park, S.-H., Ahn, H.-J. and Cho, J.-J.

TITLE Direct Submission

JOURNAL Submitted (07-SEP-2000) Microbiology, Kyung Hee University, College of Medicine, Dongdaemun-gu, Hoek1-dong 1, Seoul, Korea

FEATURES

source

1..3763

/organism="Mus musculus"

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CDS
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/cell_type="mast cell"
1..3763
/gene="Lox-1"
48..1139
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/note="Lox-1"
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/protein_id="AAC44998.1"
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2432..2437
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3721..3726
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Best Local Similarity	98.8%;	Pred. No. 3.5e-176;		
Matches 673; Conservative	0;	Mismatches 8;	Indels 0;	Gaps 0;

OY	64	aagcctaaagaggtgcccgagagaaactcaagggaaagatagacacccatcccgagag	123
Db	459	AACCTCTTCAGGGAGTCCCGAGAGAACTCAAGGAAATATGACACCATCCGGAG	518
OY	124	cttgaacgagaatccaaagacgagagagctcttcagatgatccaagaacctccaaga	183
Db	519	CTGGACGGAATATCCAAAGAGCAGGAGAGCTTCTGCAGATGATTCAGAACTCCAAAG	578
OY	184	gccctcgaagagctgcaaacctctcaagagagctcccgagagaactcaaggaaagata	243
Db	579	GCCCTGAGAGAGCTGCAAACTCTTGAGAGAGATCCCAAGAGAACTCAAGGAAAGATA	638
OY	244	gaacccctcaactctgaagctcggaaacggagaaatccaaagacgaagagagctctcaagag	303
Db	639	GACACCTTCACCTTGAAAGCTGTAAGAGAAATCCAAAGACAGAGAGAGCTTCTACAGAG	698
OY	304	aataagaacctccaaagagacccctgcagaagagctgcgaacctcttcagtgctctgcacaa	363
Db	699	AATCAGAACTCCCAAGAAAGCCCTGCAAAGAGCTGCAAACTTTTCAGGTCTTGTCCACA	758
OY	364	gactggtctctggcataaagaaaactgttaacctcttcacatgggaccttgctcgggaaaaa	423
Db	759	GACTGGCTCTGGCTTAAAGAAAACGTATACCTTTCACATGGGCCCTTTTACGTGGGAAAAA	818
OY	424	aaccggcaggaacctgcgaactcttgggttggcagattacatacaatlaagtggcagatat	483
Db	819	AACGGCGAGACCTCCCAATCTTTGGGGCCCACTTACTCAAAATTAATGTCACATATAT	878
OY	484	ctgaacatcatcttacaagaacatctcccataccactccccaattctggaatlgatctgat	543
Db	879	TTGACATTTCAATCTTACAAAGCAATTTCCCAATACCACTCCCGCTTGCGATTTGGATTGGAT	938
OY	544	cggagaagaccttggccaacacatggtcatatgggaatlgaaactctcttgaaatttcaattc	603
Db	939	CGGAGAGAGCCTGGCCCAACCATGGCTATGAGGAATGGAATCTCTTGAATTTCAATTTC	998
OY	604	tttaagaccaggggcgcttcttcaagctatatctatcaagaagaacctgtgcataacttcaa	663
Db	999	TTTAAAGCACAGGGGGCTTTTCTTACAGCTATATCTACAGGGAACGTGCATACCTTCATA	1058

Oy	664		gacggagctgtcgcgaagaacgcgccatccattcgaccatcacgatctgccaagaagg	723
Dd	1059	GACGAGCTGTGCCTTGGCGTAACAATCGCATTTCAATTTCACGATATGTCAGAAGANG	1118	
OY	724	aacaatcatlgtcaaatlttag	744	
Dd	1119	AAAAAATAATCATTGCCAAATTTTAG	1139	
RESULT	2			
ABO05900			3750 bp mRNA linear ROD 23-APR-1998	
LOCUS		Rattus norvegicus mRNA for endothelial receptor for oxidized low-density lipoprotein, complete cds.		
DEFINITION				
ACCESION		ABO05900		
VERSION		ABO05900.1 GI:30777733		
KEYWORDS		endothelial receptor for oxidized low-density lipoprotein,		
SOURCE		Rattus norvegicus (strain:SHR-SP) 13 weeks old male kidney cDNA to RRA.		
ORGANISM		Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;		
REFERENCE		1 (bases 1 to 3750)		
AUTHORS		Fujita,T. Direct Submission		
TITLE		Submitted (19-JUL-1997) Toshiro Fujita, University of Tokyo School of Medicine, Fourth Department of Internal Medicine; 3-28-6 Mejirodai, Bunkyo-Ku, Tokyo 112, Japan		
JOURNAL		(E-mail:fujita-dis@n.tokyo.ac.jp, Tel:+81-3-3943-1151, Fax:+81-3-3942-5690) 2 (sites)		
REFERENCE		Nagase,M., Hirose,S. and Fujita,T. Unique repetitive sequence and unexpected regulation of expression of rat endothelial receptor for oxidized low-density lipoprotein (LOX-1)		
BIOCHEM J.		J. 330 (Pt 3), 1417-1422 (1998)		
MEDLINE		98161826		
COMMENT		Sequence updated (11-Oct-1997).		
FEATURES		Location/Qualifiers		
CDS		1..3750 /organism="Rattus norvegicus" /strain="SHR-SP" /db_xref="taxon:10116" /sex="male" /tissue_type="kidney" /dev_stage="13 weeks old" 1..91 92..1186 /note="Lox-1"		
'UTR		/codon_start=1 /product="endothelial receptor for oxidized low-density lipoprotein"		
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/db_xref="GI:3077734"				
/translation=""MAFDDMKKPVNGOPDOCKSKPKRGHLILSTWMCAPAAYTLAILCLIVSVLTVIQQDQLDVLDVGLDKNPLMWLEMSPLSFQFFRTGVSLWMYSSTGCAALYNQGEFAENCILTARSICOKKANLLLTQ"				
ISKEQEELDONNLQEPALQAERYTESSEORELBEOJDTLSWKLNERSKEOEELLQNONSQNALORANSNGPCPDQMWRKENCYLFHGPFNNKSRENCLSADDLAQISTDYDINGVFATSCITSTSPEFMWGRLHRKNPNHLMWNENSGPSLPFOFFRTGVSLWMYSSTGCAALYNQGEFAENCILTARSICOKKANLLLTQ"				
1187..3750				
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misc_feature		/note-"ARE:A+U-rich element; motif for rapid degradation of rRNA"		
misc_feature		1730..1734		
misc_feature		/note-"ARE:A+U-rich element; motif for rapid degradation of rRNA"		
misc_feature		1738..1742		
misc_feature		/note-"ARE:A+U-rich element; motif for rapid degradation of rRNA"		

Category	Sequence	Position	Score	GC Content	Other Info
misc_feature	2236..2240	/note="ARE: A+U-rich element; motif for rapid degradation of mRNA"	2979	.2984	
polyA_signal	3610..3614	/note="ARE: A+U-rich element; motif for rapid degradation of mRNA"	3628	.3632	
misc_feature	3712..3716	/note="ARE: A+U-rich element; motif for rapid degradation of mRNA"	3731	.3736	
polyA_signal	3750	/note="13 A nucleotides"			
polyA_site					
misc_feature					
BASE COUNT	1076 a	811 c	736 g	1127 t	
ORIGIN					

Query Match	70.8%; Score 526.8; DB 10; Length 3750;
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Sequence Similarity      P-Value: 1.4e-120;
Matches 585; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

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OY	123	gctggaagaaatccaagaagcagagaggtctctgcagatgatctcagaacctccaaga	182
Db	562	GCTGAATGGGAATATCCAAAGACACAGAGAGCTTCTGCAGCAGAAATCAGAACTCCAAAG	621
OY	183	agccctgcagaagagctgtccaactcttcagagaggtcccaagaagaacttaaggagaagt	242
Db	622	AGCCTTGCAAGAAAGCTGAGAAATATTCAGAGAGTCCAGAAAGAACTGAAGAACAGAT	681
OY	243	agacacccctcaacttgaagcttgaagcagagaatccaagaagcagagagagctctcaaga	302
Db	682	AGACACCCCTCAGCTGGAAGCTAAACGAGAAATCCAAGAGCAGGAGAGACTTCTGACAGA	741
OY	303	gaatagaagaactccaagaagccctgcagaagcgtcgaactcttcaagtccctgtccaga	362
Db	742	GAAATAGAAATCTTCAGAGAGCCCTCAGAGAGCTGCAAACTCTTCAGAGTCTGTGCCAA	801
OY	363	agactggtctcgtgcataaagaagaactgtacctctccatggcgcccttggctcgggaaga	422
Db	802	AGACTGGAATCTTGCAATAAAGAAACTGTTACTCTTCCTCAATGGGCCCTTAAGTGGAAAA	861
OY	423	aaacgcgaagactcgtccaactcttgggtggccagttactactacaatthaatgltgcagatg	482
Db	862	AAGTGGGGGGAATTCCTATCTTTAGATGCCAGATTACTACAAATATGACCAACAGATGA	921
OY	483	tcctgacattcaacttaagaagaacttccatccccccctcccatcttgatggatttga	542
Db	922	TCTGAACTTCGTTCTTACAGCAACTTCCCATTTCCACTCCCAATTTGGATGGGATTAA	981
OY	543	tcggaagaagaagcctcgtgcacaacatggtctatggagagaatggaactcccttcaattccaat	602
Db	982	TGCGAAAAATCCCAACACCACTCATGGGTATGGAGAAAGCGCTCCCTTGAGTTTCAATT	1041
OY	603	ctttaagaaccaggggcgtttctttacagctatatcatcaagaagaactgtgcataacctta	662
Db	1042	CTTTTGGAGCCAGGGCGCTTCTTTACAGATGTACATCATAGGACACTGTGCATATATTTGA	1101
OY	663	agaagagagctgtctcgtcgtgaagaactgcataatgatcattcagcatatgtcagaaga	722
Db	1102	AGGAGAGAGTGTGTTGCGTGAAGAACTGCATTTTAAGTGCATTCAGCATATGTGCAGAGAA	1161
OY	723	gacaaatcaattgcasaatttag	744
Db	1162	GGCAAAATTTATGTCTAAACTGAG	1183

RESULT	3						
LOCUS	AR077718						
DEFINITION	AR077718	1318 bp	DNA	linear	PAT 31-AUG-2000		
ACCESSION	Sequence	5 from patent US 5962260.					
VERSION	AR077718						
KEYWORDS	AR077718.1	GI:10004464					
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	Unclassified.						
AUTHORS	1 (bases 1 to 1318)						
TITLE	Sawamura, T. and Masaki, T.						
JOURNAL	Recombinant production of human and bovine receptors for modified						
FEATURES	low-density lipoprotein						
source	Patent: US 5962260-A 5 05-OCT-1999;						
	Location/Qualifiers						
	1..1318						
	/organism="unknown"						
BASE COUNT	366 a	306 c	286 g	360 t			
ORIGIN							

Query Match	40.1%	Score 298.2;	DB 6;	Length 1318;
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QY 183 agccctgcagagagctgcacaactcttcagaggaqtccacagagaactcaaggaaagat 242

Dp 384 AGCCCGCAACCAAGCAGAGAGCTTCACAGGAGTCAGAAACGAACCTCAAGGAATGAT 443

Ov 3A3 agagcaccctcaccccttgaagcctgaaaccaaataccaagaagcaagaaagacgttcctacagaaa 302

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[illegible]

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503 agaacgugcaccgucacaaagaaacgucacccccc--ccacgugcacccllcgucgugaa 419
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D5 564 AGACTGGATCTGGCAGTGGAGAAACGTGTACCTATTTCCTCCGGCTCATTTAACCTGGGA 623

QY 420 aaaaaccgacaccttgcacatcttgggtgcccagttactacaataatgtgtcaga 479

Db 624 AAAGAGCCAAGAGAGTGTCTTTGGATGCCAAGTTGCTGAAATTAATAGCACAGC 683

QY 480 tgatctgacattcatcttacaagcaatttccataccaccctcccatctgtgattgatt 539

Db 684 TGATCTGGACTTCATCCAGCAAGCAATTTCCCTATTCCAGTTTCCATTCTGGATGGGCT 743

QY 540 qcatcgaaagacctggccaaccatggtctatgggagaatggaactccttgaatttca 599

Db 744 GTCTGGAGGAACCCACGCTACCCATGGCTCTGGAGGACGGTCTCTTGATGCCCA 803

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QY	/20	gaa gacaaac /30

Db 924 GAAGCAACC 934

DESCRIPTION 4

AR138263

DEFINITION Sequence 5 from patent US 6197937.

ACCESSION	ARI38263
VERSION	ARI38263.1
	GI:14479772

KEYWORDS : Unknown.
 SOURCE : Unknown.
 ORGANISM : Unknown.
 REFERENCE : Unclassified.
 1 (bases 1 to 1318)
 AUTHORS : Sawamura,T. and Masaki,T.
 TITLE : Modified low density lipoprotein receptor
 JOURNAL : Patent: US 6197937-A 5 06-MAR-2001;
 FEATURES : Location/Qualifiers
 source 1..1318
 BASE COUNT 366 a 306 c 286 g 360 t
 ORIGIN

Query Match 40.1%; Score 298.2; DB 6; Length 1318;
 Best Local Similarity 72.6%; Pred. No. 1.4e-72;
 Matches 400; Conservative 0; Mismatches 148; Indels 3; Gaps 1;

QY 183 agccctgcagagagctgcgaactcttcagagagagtcaccagagagactcaagggaagat 242
 DB 384 AGCCCGCAACAGACGAAAGACTTCCAGAGATCAGAAACGAACTCAAGCAATGAT 443
 QY 243 agagaccctacccttgaagctgaagagaatccaaagagcagagagcttctacagaa 302
 DB 444 AGAACCCTTGCTCGGAGCTGAATGAAATCCAAAGACCAATGGAACCTTCAACCA 503
 QY 303 gaatcagaacctccaagaagccctgcagaagctgcgaacttccagctctgtccaca 362
 DB 504 GAATCTGAATCTCCAGAAACACTGAAGAGAGTAGCAAAATTGTTACACTCTCTGTCGCA 563
 QY 363 agactgctctgcgataaagaactgttacctt---ccatgggcccttggctggga 419
 DB 564 AGACTGATCTGGCATGAGAAACCTGTACTATTCTTCGCGGCTCATTTAACTGGGA 623
 QY 420 aaaaaccgagcagacctgcgaactcttgggtggcagcttactcaaatatgttgaga 479
 DB 624 AAAGAGCCCAAGAGAGAGTCTTGTCTTTGATGCCAACTCTGAAATTAATAGCACAGC 683
 QY 480 tgaatcgaacatcattcaagaacatltccataccaccctcccatcttgatgatt 539
 DB 684 TGATCTGAGACTTCATCCAGACCAATTTCTTATCCAGTTTCCATTGAGATGGGCT 743
 QY 540 gcatcggaagaagcctgcgaacacatgctatggagagatggaactccttgaattca 599
 DB 744 GTCTCGAGAGAACCCAGCTACCCATGGCTCTGGAGAGAGGTTCTCTTGAATGCCCA 803
 QY 600 attcttaagacagagggtcttcttaccagctatattcaagaacacgtgcatacct 659
 DB 804 CTATTATTAGATCCGAGGCCCTGTCTCCAGACATACCTTCAAGTACCTGTGATATAT 863
 QY 660 tcaagacgagctgtgtctgcgtaaaactgcatcttaattgcatcaccatgacagaa 719
 DB 864 ACAACGAGAGCTGTATTATCGGAAAACTCATTTAGTCCCTTCAATATATGTGACGAA 923
 QY 720 gaagacaatc 730
 DB 924 GAAGCAAAACC 934

RESULT 5
 E12916 1318 bp DNA linear PAT 24-JUN-1998
 LOCUS E12916
 DEFINITION Human cDNA encoding a denatured low-density lipoprotein receptor.
 ACCESSION E12916
 VERSION E12916.1 GI:3251747
 KEYWORDS JP 1997098787-A/3.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1318)
 AUTHORS Sawamura,T. and Masaki,T.

TITLE : MODIFIED LOW DENSITY LIPOPROTEIN RECEPTOR
 JOURNAL : NIPPON CHEMIPHAR CO LTD
 COMMENT : Patent: JP 197098787-A 3 15-APR-1997;
 OS Homo sapiens (human)
 PN JP 1997098787-A/3
 PD 15-APR-1997
 PF 30-NOV-1995 JP 1995334234
 PR 30-NOV-1994 JP 94P 321705, 31-JUL-1995 JP 95P 214206 PI
 PC C12N15/09,C07H21/04,C07K14/705,C12P21/02,G01N33/53,G01N33/566,
 PC C12P21/02,
 PC C12R1.91;
 CC strandedness: Double;
 CC topology: Linear;
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 FH source 1..1318
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 FT /tissue='lung'
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 FT CDS /clone='lambda hlox-1'
 FT 127..948
 FT /product='denatured low-density lipoprotein receptor'.
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 /db_xref='taxon:9606'
 BASE COUNT 366 a 306 c 286 g 360 t
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Query Match 40.1%; Score 298.2; DB 6; Length 1318;
 Best Local Similarity 72.6%; Pred. No. 1.4e-72;
 Matches 400; Conservative 0; Mismatches 148; Indels 3; Gaps 1;

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 QY 243 agagaccctacccttgaagctgaagagaatccaaagagcagagagcttctacagaa 302
 DB 444 AGAACCCTTGCTCGGAGCTGAATGAAATCCAAAGACCAATGGAACCTTCAACCA 503
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 DB 504 GAATCTGAATCTCCAGAAACACTGAAGAGAGTAGCAAAATTGTTACACTCTCTGTCGCA 563
 QY 363 agactgctctgcgataaagaactgttacctt---ccatgggcccttggctggga 419
 DB 564 AGACTGATCTGGCATGAGAAACCTGTACTATTCTTCGCGGCTCATTTAACTGGGA 623
 QY 420 aaaaaccgagcagacctgcgaactcttgggtggcagcttactcaaatatgttgaga 479
 DB 624 AAAGAGCCCAAGAGAGAGTCTTGTCTTTGATGCCAACTCTGAAATTAATAGCACAGC 683
 QY 480 tgaatcgaacatcattcaagaacatltccataccaccctcccatcttgatgatt 539
 DB 684 TGATCTGAGACTTCATCCAGACCAATTTCTTATCCAGTTTCCATTGAGATGGGCT 743
 QY 540 gcatcggaagaagcctgcgaacacatgctatggagagatggaactccttgaattca 599
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 QY 600 attcttaagacagagggtcttcttaccagctatattcaagaacacgtgcatacct 659
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 QY 720 gaagacaatc 730

Db	924 GAAGGCAAAACC 934	
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LOCUS		
DEFINITION	Homo sapiens oxidized low-density lipoprotein receptor mRNA,	
ACCESSION	AF035776	
VERSION	complete cds.	
KEYWORDS	AF035776.1 GI:3941299	
SOURCE	.	
ORGANISM	human.	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
TITLE	Ll,X., Bouzyk,M.M. and Wang,X.K. Human oxidized low density lipoprotein receptor: characterization of the full length cDNA sequence and assignment to human chromosome 12p13.1-12.3	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 2067)	
AUTHORS	Wang,X.K.	
TITLE	Direct Submission	
JOURNAL	Submitted (24-NOV-1997) Cardiovascular Pharmacology, Smithline Beecham Pharmaceuticals, 709 Swedeland Road, UW2511, King of Prussia, PA 19406, USA	
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Oy	183 agccctgagagagctgtcaaaccttccagagagctccacagagaactcaaggaaagt 242	
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Oy	243 agacacctcaaccttggaagctggaagagaatccaagaagcagagagctttcacgaa 302	
Db	364 AGAAMACCTTGCTCGGAAGCTGTAATGATAAATCCAAAAGCAAAATGTACACACCA 423	
Oy	303 gaatcagaacctccaagaagccctgcgaagagctgcaaacttttcagtlcctgtccaca 362	
Db	424 GAAATGTGAATCTCCNAAGAACCTGAGAAGAGTAGACAATTGTTGAGCTCCTGTGCCA 483	
Oy	363 agactggctctggcataaagaaaactgttaactctt---caatgggcccttggctggga 419	
Db	484 AGACTGGATCTGGCATGAGAAATGTTTACTATTCTTCGCGGCTCATTTAACTGGGA 543	
Oy	420 aaaaaaccggcagactccaactcttggcgggccaggttactaacaattaatgtgtaga 479	
Db	544 AAAGAGCCAAGAGAGAGTCTGTCTTTTGGATGCCAAGTGTCTGAAATTAATAGCACAGC 603	

QY	480	tgatcgcagctcaattcctaagaacattccatacccaccgcccatctgattgaatt	539
Db	604	TGATCTGCAGCTTCAATCCACGAAGAATTTCCTAATCCAGTTTCCATTCTGGATGGGECT	663
QY	540	gcattcgagaagaagccctggccaacctgactgtctatggaatgaaactcccttgaatttca	599
Db	664	GTCCTCGAGGAAACCACCACACTACCATAGGCTCTGGGAGGACGGTTCTCCTTGATGATCCCCA	723
QY	600	attccttaagaaccaaggcgctttcttcacagctalatcatcaagaacaactgtgcatacct	659
Db	724	CTTATTATTAGATGCCAGGCGCTGTCTCCACAACATATCCCTTCAGGTACTGTGCATATAT	783
QY	660	tcaagacggagcgtgctgcctgaaaactgatcatattcatcattcaagcattgcagaa	719
Db	784	ACAACGAGGAGCTGTTTATGCGAAAACATGCAATTTACTCTCTTCAGTAATATGTCAGAA	843
QY	720	gaagacaacatc 730	
Db	844	GAAGCAAAACC 854	
RESULT	7		
LOCUS	ABO10710	2463 bp	mRNA linear PRI 03-FEB-1998
DEFINITION	Homo sapiens mRNA for lectin-like oxidized LDL receptor, complete cds.		
ACCESSION	ABO10710 D89050		
VERSION	ABO10710.1 GI:2828355		
KEYWORDS	lectin-like oxidized LDL receptor; LOX-1.		
SOURCE	Homo sapiens lung cDNA to mRNA.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 2463)		
TITLE	Sawamura,T.		
JOURNAL	Direct Submmission		
	Submitted (22-JAN-1998) Tatsuya Sawamura, Kyoto University,		
	Department of Pharmacology, Faculty of Medicine, Yoshidakonocho,		
	Sakyo-ku, Kyoto, Kyoto 606, Japan		
	(E-mail:sawamura@tour.med.kyoto-u.ac.jp, Tel:81-75-753-4393,		
	Fax:81-75-753-4402)		
REFERENCE	2 (sites)		
AUTHORS	Sawamura,T., Kume,N., Aoyama,T., Moriwaki,H., Hoshikawa,H.,		
	Alba,Y., Tanaka,T., Miwa,S., Katsura,Y., Kita,T. and Masaki.T.		
TITLE	An endothelial receptor for oxidized low-density lipoprotein		
JOURNAL	Nature 386 (6620), 73-77 (1997)		
MEDLINE	97205278		
COMMENT	On Feb 3, 1998 this sequence version replaced gi:1902983.		
FEATURES	Db89050: Submitted (12-Nov-1996).		
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	/db_xref="GI:1902984"		
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	KEMETELARKNKESKDMENHLHGNIINLEOTLRKANCSAPCPDDMIWHGENCYLFSS		
	GSFMWEKSQEKSLDAIKLKINSTALDLPTQQAISVSPPFWMGISRNSYPWLMRE		
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QY 720 gaagacaatc 730
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 Db 853 GAGGCAAC 863

RESULT 9
 AB018668
 LOCUS
 DEFINITION Sus scrofa mRNA for lectin-like oxidized LDL receptor-1, complete cds
 1578 bp mRNA linear MAM 08-MAY-2001

ACCESSION AB018668
 VERSION AB018668.1 GI:6682817
 KEYWORDS lectin-like oxidized LDL receptor-1.
 SOURCE Sus scrofa aortic endothelial cells cDNA to mRNA.
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

REFERENCE 1 (sites)
 AUTHORS Chen, M., Narumiya, S., Masaki, T. and Sawamura, T.
 TITLE Conserved C-terminal residues within the lectin-like domain of LOX-1 are essential for oxidized low-density-lipoprotein binding
 JOURN. Biochem. J. 355 (Pt 2), 289-296 (2001)
 MEDLINE 21181560
 REFERENCE 2 (bases 1 to 1578)
 AUTHORS Sawamura, T.
 TITLE Direct Submission
 JOURN. Submitted (14-OCT-1998) Tatsuya Sawamura, National Cardiovascular Center Research Institute, Department of Bioscience, 5-7-1 Fujishirodai, Suita, Osaka 565-8565, Japan (E-mail: sawamura@ri.ncvc.go.jp, Tel: 81-6-833-5012(ex. 2518), Fax: 81-6-872-7485)

FEATURES
 source Location/Qualifiers
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BASE COUNT 415 a 351 c 321 g 491 t
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Query Match 39.5%; Score 293.6; DB 4; Length 1578;
 Best Local Similarity 71.8%; Pred. No. 2.7e-71;
 Matches 399; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

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 Db 302 AGCCGAGCGCCAGCGGAAATCTTCCAGATGACAAAGGAACTCAGAAATGAT 361
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QY 243 agacaccccaactcgaagcgaagaaatcaagagagagagagctctcacaaga 302
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 Db 362 AGAAGCTCTGCGCCCAAAATTCGATGAAATCCAAAGAACTGATGAGACTTCACACAGA 421
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QY 303 gaataagaacctccaagaagccctcgaagagctcgaactttcaggtcctgtccaca 362
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 Db 422 GAAGTGTATCTTCAAAAAAGCTCTGAGAAAGCGGCAAACTTTCAGGTCTTGTCCCA 481
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QY 363 agactggctctggcgaataagaactgttac---ctctccatgggccccttgctggaga 419
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 Db 482 AGACTGGCTCTGGCATGAAAGAACTGTACAAATTTCTCTGCGCCCTTATGTTGGGA 541

QY 420 aaaaaaccgagacctgcgaactcttggtggtgcagagtactacaataatggtgcaga 479
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 Db 542 AAAAAGCCGAGAGACTGCTGTTTGATGATCCCAAGCTGGAAGATTAAAGACAGCA 601
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QY 480 tgatctgacatcattcattcaagaagaattcccatccaccctcccatcttgatgatt 539
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 Db 602 CGATCTGGAATTCATCCAGCAACCAACATCGCCATTCAGATTCCCATCTCGATGGGGTT 661
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 Db 662 ATCTCTGAGAGAACCAACAACTCATGCTGTGGAGAGAGGCTACTCTTTGATGCCCA 721
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 Db 842 GAGGCGAATCTCTTG 857

RESULT 10
 DB89049
 LOCUS
 DEFINITION Bos taurus mRNA for lectin-like oxidized LDL receptor, complete cds.
 1879 bp mRNA linear MAM 07-FEB-1999

ACCESSION DB89049
 VERSION DB89049.1 GI:1902981
 KEYWORDS lectin-like oxidized LDL receptor; LOX-1.
 SOURCE Bos taurus aortic endothelial cells cDNA to mRNA, clone: pBLOX-1.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 1879)
 AUTHORS Sawamura, T.
 TITLE Direct Submission
 JOURN. Submitted (12-NOV-1996) Tatsuya Sawamura, Kyoto University, Department of Pharmacology, Faculty of Medicine, Yoshida-kono-e-cho, Sakyo-ku, Kyoto, Kyoto 606, Japan (E-mail: sawamura@four.med.kyoto-u.ac.jp, Tel: 81-75-753-4477, Fax: 81-75-753-4402)

REFERENCE 2 (bases 1 to 1879)
 AUTHORS Sawamura, T., Kume, N., Aoyama, T., Moriaki, H., Hoshikawa, H., Aiba, Y., Tanaka, T., Miwa, S., Katsura, Y., Kita, T. and Tomoh, M.
 TITLE A novel endothelial receptor for oxidized low density lipoprotein
 JOURN. Unpublished (1996)

REFERENCE 3 (sites)
 AUTHORS Sawamura, T., Kume, N., Aoyama, T., Moriaki, H., Hoshikawa, H., Aiba, Y., Tanaka, T., Miwa, S., Katsura, Y., Kita, T. and Masaki, T.
 TITLE An endothelial receptor for oxidized low-density lipoprotein
 JOURN. Nature 386 (6620), 73-77 (1997)
 MEDLINE 97205278

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 /product="lectin-like oxidized LDL receptor"
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Qy      660 tcaagacgagctgtgtcgtcgaagaactgcatctcaattcgaactcgaatagtcagaa 719
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RESULT 13
LOCUS   E12914      1897 bp      DNA      linear      PAT 24-JUN-1998
DEFINITION Bovine cDNA encoding a denatured low-density lipoprotein receptor.
ACCESSION E12914
VERSION   E12914.1 GI:3251745
KEYWORDS  JP 1997098787-A/1.
SOURCE    cow.
ORGANISM  Bos taurus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
           Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 1897)
AUTHORS  Sawamura,T. and Masaki,T.
TITLE     MODIFIED LOW DENSITY LIPOPROTEIN RECEPTOR
JOURNAL  Patent: JP 1997098787-A 15-APR-1997;
          NIPPON CHEMIPHAR CO LTD
COMMENT   OS Bos taurus (bovine)
          PN JP 1997098787-A/1
          PD 15-APR-1997
          PF 30-NOV-1995 JP 1995334234
          PR 30-NOV-1994 JP 94P 321705, 31-JUL-1995 JP 95P 214206 PI
          SARAWURA TATSUYA, MAZAKI TOMOO
          PC C12N15/09,C07H21/04,C07K14/705,C12P21/02,G01N33/53,G01N33/566,
          PC C12P21/02,
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          FT /cell_type='vascular endothelial cells' FT

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Query Match      38.6%; Score 287.2; DB 6; Length 1897;
Best Local Similarity 71.0%; Freq. No. 1.7e-69;
Matches 395; Conservative 0; Mismatches 158; Indels 3; Gaps 1;

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Qy      420 aaaaaccgagagacgtgcgaactcttgggtggcgaagtactacaataatggtgcga 479
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Qy      480 tgatctgacatctctacaaagcaattccatccacccctccatctgattgatt 539
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Qy      540 gcatcgaagaagcctgagcaacatggtctatgggagaatggaactccttgaatttca 599
Db      640 GTCAATGAGAAACCAATTAATCTGCTGGTGGAGAGATGTTACTCTTGACGCCCA 699
Qy      600 attcttaagcagagcgttcttcttcaagctatattcaagaacatggtcattact 659
Db      700 CTGTGTTGAATTCAGGAGCTGTTCCCGATGATATCTTCAGGACCTGTCATTAAT 759
Qy      660 tcaagacgagctgtgtcgtcgaagaactgcatctcaattcgaactcgaatagtcagaa 719
Db      760 TCAAGGGGAACCTGTTTGTGTAAGAACTGCATTTTAATGATATGTCAGAA 819
Qy      720 gaagacaactcatttg 735
Db      820 GAAGCGCAATCTATTG 835

RESULT 14
LOCUS   AR077717      1906 bp      DNA      linear      PAT 31-AUG-2000
DEFINITION Sequence 3 from patent US 5962260.
ACCESSION AR077717
VERSION   AR077717.1 GI:10004463
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE 1 (bases 1 to 1906)
AUTHORS  Sawamura,T. and Masaki,T.
TITLE     Recombinant production of human and bovine receptors for modified

```


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[illegible]


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QY 303 gaatcagaacctcccaagaagccctgcgaagctgcgaaccttctcaggtctgtccaca 362
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Db 504 gaatctgatactccaagaacactgaagagtgtagcaattgttcagctctgtccgca 563
QY 363 agactggtcttggtctaaagaactgttacctt---ccatggcccttggctggga 419
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Db 564 agactggaactctgcgaatgagaactgttacctattcttcctgggctcatttaactggga 623
QY 420 aaaaacggcgagacctccaactcttgggtggccagttactacaataatggtgcaga 479
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QY 480 tgatctgacatcattcttaacaagaacttcccataccacccctccatctggatggatt 539
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Db 684 tgatctgactcttccagcaagaacttccattccattccagtttccattctgtatgggct 743
QY 540 gcatcggaagaagcctgcgcacacatcgtctatggagaatggaactccttgaatttca 599
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Db 744 gctcggaggaaccccaactaccatgctcgtggagagcgttctccttggatgccca 803
QY 600 attcttaagaccagggcgcttcttcttaagctatattcaagaactgtgcatact 659
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Db 804 ctatttgagctcgaagcgctgtctccagacacatacccttcaggtaccctggcatatat 863
QY 660 tcaagacgagagctgtgttcgtctgaagaactgcatcttaattgcatcagcatatgcagaa 719
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Db 864 acaagagagagctgttattgctgcgaagaactgcatctttagctgcttcagtatatgcagaa 923
QY 720 gaagacaact 730
    ||||| |||||
Db 924 gaaggaacaac 934

RESULT 3
AA88527
ID AA88527 standard; DNA; 1318 BP.
AC AAX88527;
XX
XX 10-SEP-1999 (first entry)
DE Human LDL receptor encoding DNA.
XX
XX Human; LDL; denatured; oxidised; arteriosclerosis; hyperlipidaemia;
KW low density lipoprotein; receptor; detection; immunoglobulin;
XX fusion protein; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1..126
FT 5'UTR
FT CDS 127..948
FT /*tag= a
FT /*tag= b
FT 949..1318
FT 3'UTR /*tag= c
FT
FT
PN MO932520-A1.
XX
XX 01-JUL-1999.
PD
XX
XX 18-DEC-1998; 98WO-JP05744.
XX
XX 16-DEC-1998; 98JP-0358170.
PR 19-DEC-1997; 97JP-0364981.
PR 09-DEC-1998; 98JP-0349648.
XX
XX (NTSB ) JAPAN TOBACCO INC.
PA
XX
XX Kakutani M, Masaki T, Sawamura T;
PI
XX WPI: 1999-416906/35.
DR
DR P-PSDB; AAY24151.
```

```
XX
XX Fusion peptide for assay of oxidized LDL and for therapeutic use
PI
XX
XX Disclosure: Page 84-87; 105pp; Japanese.
PS
XX
XX The present invention describes a fusion peptide which consists of the
CC extracellular domain of a mammalian oxidized LDL (low density
CC lipoprotein) receptor, fused to a partial heavy chain of a mammalian
CC immunoglobulin containing all or part of the constant region. Oxidized
CC LDL is a denatured form of LDL occurring in patients having
CC arteriosclerosis or hyperlipidaemia, and the fusion peptide can be
CC used for the assay of oxidized LDL in biological samples from such
CC patients, for the diagnosis of the disorders. It can also be used
CC therapeutically for the prevention and treatment of arteriosclerosis and
CC hyperlipidaemia. The present sequence encodes the human LDL receptor.
XX
SQ Sequence 1318 BP; 366 A; 306 C; 286 G; 360 T; 0 other;
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Query Match 40.1%; Score 298.2; DB 20; Length 1318;
Best Local Similarity 72.6%; Pred. No. 1,1e-76;
Matches 400; Conservative 0; Mismatches 148; Indels 3; Gaps 1;

QY 183 agccctgcagagagctgcgaactctcagagagctccagagagaactcaaggaagaat 242
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Db 384 agcccgcaacaagaagaagcttcaagagtcagagaagaacgaactcaagaagaatgat 443
QY 243 agacacctcaactctgaagctgaacgaagaatccaagaagcagaagagctctcagaa 302
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 444 agaaacctgtctcgaaactgtaatgaaatccaagaagcaaatgaaactcacaccaca 503
QY 303 gaatcagaacctccaagaagccctgcgaagagctcgaacttccagttcctgtgccaca 362
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Db 504 gaatctgaatctccaagaagaacactgaagagtgagaatgttgaactcctgtccgca 563
QY 363 agactggtctgcgaatgaagaactgttacctt---ccatggcccttggctggga 419
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Db 564 agactggaactgcgaatgagaactgttacctattcttcctcgggtcatttaactggga 623
QY 420 aaaaacggcgagacctccaactcttgggtgggtgcagttactacaataatggtgcaga 479
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 624 aaagggccaagaagaagctgtctgtcttgatgagcaagttgcaaatgaatgaacagc 683
QY 480 tgatctgacatcattcttaacaagaacttcccatccacccctccatctgtgattggatt 539
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Db 684 tgatctgactcttccagcaagaacttccattccatccagtttccattctgtatgggct 743
QY 540 gcatcggaagaagcctgcgcacacatcgtctatggagaatggaactccttgaatttca 599
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Db 744 gctcggaggaaccccaactaccatcagctcgtgcgagagcgttctccttgaatgccca 803
QY 600 attctttaaagaccagggcggttcttcttaagctatattcatcaagaactgtgcatact 659
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Db 804 ctatttgagctcgaagcgctgtctccagacacatcccttcaggtactgtgcataatat 863
QY 660 tcaagacgagagctgtgttcgtctgaagaactgcatcttaattgcatcagcatatgcagaa 719
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Db 864 acaagagagagctgttattgctgcgaagaactgcatctttagctgcttcagtatatgcagaa 923
QY 720 gaagacaact 730
    ||||| |||||
Db 924 gaaggaacaac 934

RESULT 4
AAF90651
ID AAF90651 standard; DNA; 2463 BP.
AC AAF90651;
XX
XX 04-MAY-2001 (first entry)
DT
XX Human secreted protein encoding DNA, SEQ ID NO:120.
DE
```

XX Secreted protein; transmembrane protein; human; drug screening;
 KM activity modulator; expression modulator; cancer; immunological disorder;
 KM cytosolic; immunomodulatory; gene therapy; ds.
 XX Homo sapiens.
 OS
 PN WO200109162-A2.
 PD 08-FEB-2001.
 XX
 PF 31-JUL-2000; 2000MO-US20935.
 XX
 PR 30-JUL-1999; 99US-0365164.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 PI Fraser CC, Sharp JD, Kirst SJ, Barnes TM, Wrighton N, Myers PS;
 PI Pan Y;
 DR WPI; 2001-138647/14.
 XX
 XX Nucleic acids encoding secreted TANGO and MANGO polypeptides, useful
 PT for the prevention, diagnosis and treatment of, e.g. cancers and immune
 PT disorders -
 PS Disclosure; Page 272; 332pp; English.
 XX
 XX The invention relates to novel secreted/transmembrane proteins, and
 CC nucleic acids encoding them. The novel proteins are designated TANGO 339,
 CC TANGO 353, TANGO 358, TANGO 365, TANGO 368, TANGO 369, TANGO 383, TANGO
 CC 393, TANGO 402, MANGO 346 and MANGO 349 and are of human origin, and a
 CC murine TANGO 393 is also included within the scope of the invention. The
 CC invention also encompasses fragments and variants of the proteins of the
 CC invention, and nucleic acids encoding them. The invention additionally
 CC relates to host cells comprising a nucleic acid of the invention; methods
 CC for the production of a protein of the invention; an antibody specific
 CC for a protein of the invention; methods for detecting a protein or
 CC nucleic acid of the invention; and methods of identifying agents which
 CC bind to or modulate the activity of a protein of the invention. The novel
 CC secreted proteins, nucleic acids encoding them, and antibodies against
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate expression or activity of the secreted
 CC proteins. The secreted proteins of the invention may also be used to
 CC identify modulators of expression or activity, which may be useful in
 CC the treatment of disorders associated with the proteins of the
 CC invention e.g., cancers and immunological disorders. The present
 CC sequence represents DNA encoding a human secreted protein.
 X
 Q Sequence 2463 BP; 734 A; 518 C; 467 G; 744 T; 0 other;

Query Match 40.1%; Score 298.2; DB 22; Length 2463;
 Best Local Similarity 72.6%; Pred. No. 1.5e-76;
 Matches 400; Conservative 0; Mismatches 148; Indels 3; Gaps 1;

QY 183 agccctgcagagagctgcgaactcttcagagagctccagagagaactcaagggaagat 242
 DB 319 agcccgcaacaagaagagcttcacagagctcagaaacgaactcaagaagaatgat 378
 QY 243 agacaccctcacttggaagtgaagcagaagaatcaagaagcagaagagcttcaagaa 302
 DB 379 agaaacctgtcgcgaagctgaatgaatccaaagagaatgaatgaatccaccaca 438
 QY 303 gaatcagaacctcagaagccctgcgaagagctgcaaaacttcagctcgtccaca 362
 DB 439 gaatcgaatctccaagaacactcgaagagagtagcaaatgttcgcttcgtccgca 498
 QY 363 agactgctcgtgcataaagaactgttaacctt--ccatgggaccttggctggga 419
 DB 499 agactgatactgcagcagaaactgttaccattctcctggcgccatttaactggga 558
 QY 420 aaaaaaccggcagagctgcgaatcttgggtggcaggttactactcaaatatagtgacaga 479

DB 559 aaagagcccaagagaagctgtcttcttcttgatgccaagctgtaaaatcaatcacagc 618
 QY 480 tgatcgaatcatcttaacgaatccatccacacccctccctcgtgattgatt 539
 DB 619 tgatcgtgaactcatccagcaagaatctctcatcttcaggttccattcctcgtatgggct 678
 QY 540 gcatcggaaagaagctgtgcacaacatgctatggaagaatgaaactccttgaattca 599
 DB 679 gtctcgaggaagaccaccatgctcctcgtggaagagcttctccttcttgatgccca 738
 QY 600 atctttaaagaaccaggggcttcttcttacagctatattcaagaacgtgcatcct 659
 DB 739 ctatttaagagctcggagcgctgtctccagaacatcaccctcaggtaacctgcatat 788
 QY 660 tcaagcagagctgtgtcgtgaacatgcatcattcaatcagcatatgcaaga 719
 DB 799 acaacgagagagctgttattatgcgaaactgcatlcttgcgtccttcagatatagtcaga 858
 QY 720 gaagacaatc 730
 DB 859 gaagcaaac 869

RESULT 5
 AAH47105
 ID AAH47105 standard; cDNA; 2468 BP.
 XX
 XX AAH47105;
 AC
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Human LOX-1 polypeptide encoding cDNA.
 XX
 KM LOX-1; LDL; monoclonal antibody; low density lipoprotein; human;
 KM atherosclerosis; cardiovascular; kidney disease; inflammatory disorder;
 KM leukocyte; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 5'UTR 1..61
 FT /*tag- a
 FT 62..863
 FT /*tag- b
 FT 884..2468
 FT 3'UTR /*tag- c
 FT
 XX
 PN WO200164862-A1.
 PD
 PD 07-SEP-2001.
 PF 02-MAR-2001; 2001MO-JP01636.
 PR 02-MAR-2000; 2000JP-0057745.
 PR 31-OCT-2000; 2000JP-033116.
 PA (ABGE-) ABGENIX INC.
 PI Kobayashi Y, Tsuji H, Kamada M, Sawamura T;
 DR WPI; 2001-565503/63.
 DR P-PSDB; AAB85869.
 PT Human monoclonal antibodies recognizing oxidized low density
 PT lipoprotein receptor for treatment of atherosclerosis and
 PT cardiovascular and kidney diseases -
 PS Disclosure; Page 87-92; 131pp; Japanese.
 XX
 XX The invention provides human monoclonal antibodies and their fragments
 CC binding to human oxidized low density lipoprotein (LDL) receptor (LOX-1),
 CC and inhibiting intracellular binding of the receptor to oxidized LDL.

FT	3' UTR	/*tag= b
FT		870..1578
FT		/*tag= c
XX		
PN	WO200164862-A1.	
XX		

02-MAR-2001; 2001WO-JP01636.
02-MAR-2000; 2000JP-0057745.

(ABGE-) ABGENIX INC.

Kobayashi Y, Tsuji H, Kamada M, Sawamura T;

WPI: 2001-565503/63.
P-PDB; AAB85872.

Human monoclonal antibodies recognizing oxidized low density lipoprotein receptor for treatment of atherosclerosis and cardiovascular and kidney diseases -

Disclosure: Page 111-115; 131pp; Japanese.

The invention provides human monoclonal antibodies and their fragments binding to human oxidized low density lipoprotein (LDL) receptor (LOX-1), and inhibiting intracellular binding of the receptor to oxidized LDL. Drug compositions containing the Mab are useful in the treatment and prevention of atherosclerosis, cardiovascular and kidney diseases, inflammatory disorders and infiltration of leukocytes. The present sequence represents a S. scrofa LOX-1 polypeptide encoding cDNA.

SQ Sequence 1578 BP; 415 A; 351 C; 321 G; 491 T; 0 other:

Query Match 39.5%; Score 293.6; DB 22; Length 1578;
Best Local Similarity 71.8%; Pred.No. 2.6e-75;
Matches= 399; Conservative 0; Mismatches 154; Indels 3; Gaps 1.

DY 183 agccctgcagaagcgtgcaactcttcagagaggatcccacgaagaagtccaagggaaagat 242
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DB 302 agccccagcgccacggcygaaaatacttccaccagattcacaaaaggaaacttacagaatat 361

Oy 243 agaacacctcaccttgaaagctgaacgagagaatcaaagagcgagggaagttctaaca 302
 ||| || || ||| ||| |||
Db 362 agaaactcttgcacacaattgatgaaaaaatccacagaagaactcgatggagcttccaagaa 421

Oy 303 gatacgaacttcacaagaagccctlgaagaagctlgaacttltaagttcattgccaca 362
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QY 363 agacgtgctcctggcataagaactgttac---ctcttcgatggcccttgctggga 419
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 482 agactggcctctgcagaaactglttaacaatttctcttggcccatttagttggga 541

QY 420 aaaaaaccgycagacctggcaactcttggtygtgcagtactacaataatgtygcaga 479
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 542 aaaagccggysgaactgtcttcttgatgccccactgcgtgaagattaagcacaga 601

QY 480 tcatcgcaattcatcttcaagaacttcccatcacctcccatcttgatggatt 539
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 602 cgatcgtggaattcatccaagaacaacctgccatccagtctccatcttgatggatt 661

QY 540 gcatcggaagaagctgtgccaacatgctatgaggaaatggaactccttgaattuca 599
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 662 atctcggagaaacccaacaactcagctctcggysgagcgytactccbtatgccoca 721

QY 600 attctttaagacaagagcgttctctttaagatatctatcaagaacatgfatcact 659
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Db 722<cttgtttaactccagsgcgtcttcccaaatgtatctctcaagcactcgtgcatat 781

QY	720	gaagacaatcatcttg	735
Db	842	gaaggcgaaatctcttg	857

RESULT 7

AAx88529
ID AAx88529 standard; DNA; 1335 BP.
v

DE Bovine LOX-1 extracellular region/human IgG1 Fc region chimeric protein
XX
LDL, denatured; oxidised; arteriosclerosis; hyperlipidaemia;
KW low density lipoprotein; receptor; detection; immunoglobulin;
KW fusion protein; chimeric protein; ss.
XX

05	Chimeric - Bos sp.
05	Chimeric - Homo sapiens.

PN W09932520-A1.

01-JUL-1999

PF 18-DEC-1998; 98WO-JP05744.

PR 16-DEC-1998; 98JP-0358170.
PR 10-DEC-1997; 97TD-0364001

PR 09-DEC-1998; 98JP-0349648.

PA (NISB) JAPAN TOBACCO INC.
xx

PI Kakutani M, Masaki T, Sa-
vy

DR WPI; 1999-418906/35.
DB B-PCPB: 2AX24153

XX	Enfermedades
DFE	Enfermedades

XX
PS
Claim 14. Page 70

the present invention describes a function controller

extracellular domain of a mammalian ox

Immunoglobulin comprising all or part of the constant region. Oxidized LDL is a denatured form of LDL occurring in patients having arteriosclerosis or hyperlipidaemia, and the fusion peptide can be used for the assay of oxidized LDL in biological samples from such patients, for the diagnosis of the disorders. It can also be used therapeutically for the prevention and treatment of arteriosclerosis and hyperlipidaemia. The present sequence encodes a chimeric protein comprising the bovine LOX-1 extracellular region and the human immunoglobulin IgG1 Fc region.

Sequence 1335 BP; 372 A; 371 C; 324 G; 268 T; 0 other;

Query Match	38.68;	Score 287.2;	DB 20;	Length 1335;
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Db	126	agaaccccttgcacaaagctgtgatgaattccaagaataatgtgaactacgcga	185
Oy	303	gaatcagaacctccaagaagccctgcgaagaagctgcgaacttttcaagtcctgtccaca	362
Db	186	gaacctgaattccaagaagttctgnaagagcgacgaacaactatcagttccttgtccca	245
Oy	363	agactgctctgcgataaagaanaactgttacc---cttccatgtagcccttgcgtgga	419
Db	246	agactggtctcgtgatgagaagaacctgttaccaattttccctctgctcctttaattgga	305
Oy	420	aaaaaacgcgcagacctgtccaaacttttgggtgtgcccagttactacaatttaatgtgcaga	479
Db	306	aaaaagccagaggaactgtctgtcttfgatgcccacttgtcgaagattaatgcacaaga	365
Oy	480	tgaatgcatacttacttcaagaagaatttcccacacacccctcccatcttgcgaattgat	539
Db	366	tgaactggaattcatccagacgaagaatgatgtgccacttccagtttccctctcgtgatgggtc	425
Oy	540	gcatacgaagaagcctgtgcacaacatgagctatagggaatggaactcccttgaatttca	599
Db	426	gtcaatgagggaacccaattactcgtgtgttggaaagatgtaacttcccttgcgcacca	485
Oy	600	attccttaagaaccagggcgttcttcttaagcgtatcttcatcaagaacatgcataccct	659
Db	486	cttgtttagaattcaaggagactgtttcccgatgtatcccttcaggagccgtgcataat	545
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Db	546	tcaagagggaactgttttctgtgaanaactgatttaactgaactcagtaactatgtcgaag	605
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Db	606	gaaggcgaactcattg 621	

RESULT

AAH47106
ID AAH47106 standard; cDNA; 1879 BP

AC AAH47106;

DT 30-NOV-2001 (first entry)

Bovine LOX-1 polypeptide encoding cDNA

KW LOX-1; LDL; monoclonal antibody; low density lipoprotein; human;

leukocyte; bovine; ss.

OS Bos taurus.

EH	Key	Location/qualifiers
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ET	/*tag=	a
EM		
CDC	35	847

3 / 11m7

xy **xy**

PN MO200164862
xy

PD 07-SEP-2001
xy

02-MAR-2001
PE
XXPR 02-MAR-2000
PR 31-OCT-2000XX
X

XX
XX
XX

DR P-PSDB; AAB85870.
 XX Human monoclonal antibodies recognizing oxidized low density
 PT lipoprotein receptor for treatment of atherosclerosis and
 PT cardiovascular and kidney diseases
 XX
 PS Disclosure; Page 94-98; 131pp; Japanese.
 XX
 CC The invention provides human monoclonal antibodies and their fragments
 CC binding to human oxidized low density lipoprotein (LDL) receptor (LOX-1),
 CC and inhibiting intracellular binding of the receptor to oxidized LDL.
 CC Drug compositions containing the Mab are useful in the treatment and
 CC prevention of atherosclerosis, cardiovascular and kidney diseases,
 CC inflammatory disorders and infiltration of leukocytes. The present
 CC sequence represents a bovine LOX-1 polypeptide encoding cDNA.
 XX
 SQ Sequence 1879 BP; 520 A; 349 C; 353 G; 657 T; 0 other;

Query Match 38.6%; Score 287.2; DB 22; Length 1879;
 Best Local Similarity 71.0%; Pred. No. 2.1e-73;
 Matches 395; Conservative 0; Mismatches 158; Indels 3; Gaps 1;

QY 183 agccctgcagagagctgcaactcttcagagagagtcacagagaagactcaagggaagat 242
 DB 280 agccagcgccgcatcagaagaatctgcccagagatgcacagagaagactcaagaatgat 339
 QY 243 agacacccctcccttgaaagctgaagcagaatcccaagaagagagagctcttcagaa 302
 DB 340 agaaaccccttgccacaagctgagatgagaatcccaagaatgaactcacccgcca 399
 QY 303 gaatcagaacctccaagaagcctgcgaagagctgcaactttcaggtcctgtccaca 362
 DB 400 gaactgaatctccaagagagcttcgaaagagcgaacactatcaggtcctgtcccca 459
 QY 363 agactgctctgcgataaagaactgttacc---tcttcataggcccttgctgctgga 419
 DB 460 agactgctctgcgataaagaactgttaccacttccctgctctttaaattggga 519
 QY 420 aaaaaacggcagaccttcgaactcttggtggtgagcttactacaataatggtgcaga 479
 DB 520 aaaaaacggcagagacctgtgcttcttgatgacccaacttgatgaataatgacacga 579
 QY 480 tgactcgaatcattcattacaagaacttccatcacacccctccatctgattgatt 539
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 DB 640 gtcatacggaagaacccaactactcgtgcttggtggaagatggtactccttgaagcccca 699
 QY 600 attcttaagaccagggcgcttcttcaagctatcatcatcacaagaactggtactact 659
 DB 700 ctgtcttaagatcagaagagctgttccgcatgtatcccttcagggacttgatataat 759
 QY 660 tcaagacggaagctgtctgcctgaaactgcatcattcaattgcatcagcatatgacaga 719
 DB 760 tcaagaggaagactgttctgtgaaactgcatcattcaattgcatcagcatatgacaaa 819
 QY 720 gaagacaatcatcttg 735
 DB 820 gaagcggaatcatctg 835

RESULT 9

AAT32576
 ID AAT32576 standard; DNA; 1897 BP.

AC AAT32576;

XX 29-OCR-1996 (first entry)

XX Low density lipoprotein receptor coding sequence.

XX LDL; low density lipoprotein; receptor; bovine; assay; detection;
 KW recombinant production; haemangioendothelial cell; ss.
 XX
 OS Bos taurus.

XX
 FH Key Location/Qualifiers
 FT 5'UTR 1..34
 FT CDS 35..847
 FT /*tag= a
 FT /*tag= b
 FT /product= LDL_receptor
 FT 3'UTR 848..1897
 FT /*tag= c
 FT polyA_signal 1859..1864
 FT /*tag= d
 FT misc_feature 1880..1897
 FT /*tag= e
 FT /*note= "polyA site"

W09617058-A1.

06-JUN-1996.

30-NOV-1995; 95WO-JP02444.

31-JUL-1995; 95JP-0214206.

30-NOV-1994; 94JP-0321705.

(NICH) NIPPON CHEMIPHAR CO.

Masaki T, Sawamura T;

WPI: 1996-277778/28.

P-PSDB; AAR9586.

PT DNA encoding denatured low-density lipoprotein receptor of mammalian
 PT haemangioendothelial cells - useful for generating antibodies for
 PT use in detection of LDL in biological samples

PS Claim 1; Page 22-26; 44pp; Japanese.

CC The present sequence is that of bovine DNA which encodes a denature low
 CC density lipoprotein (LDL) receptor isolated from haemangioendothelial
 CC cells. The DNA is useful for the production of the receptor protein in
 CC transformed hosts. Antibodies to the protein are useful in detection
 CC and assays of LDL in biological samples.

SQ Sequence 1897 BP; 538 A; 349 C; 353 G; 657 T; 0 other;

Query Match 38.6%; Score 287.2; DB 17; Length 1897;
 Best Local Similarity 71.0%; Pred. No. 2.1e-73;
 Matches 395; Conservative 0; Mismatches 158; Indels 3; Gaps 1;

QY 183 agccctgcagagagctgcaactcttcagagagagtcacagagaagactcaagggaagat 242
 DB 280 agccagcgccgcatcagaagaatctgcccagagatgcacagagaagactcaagaatgat 339
 QY 243 agacacccctcccttgaaagctgaagcagaatcccaagaagagagagctcttcagaa 302
 DB 340 agaaaccccttgccacaagctgagatgagaatcccaagaatgaactcacccgcca 399
 QY 303 gaatcagaacctccaagaagcctgcgaagagctgcaactttcaggtcctgtccaca 362
 DB 400 gaactgaatctccaagagagcttcgaaagagcgaacactatcaggtcctgtcccca 459
 QY 363 agactgctctgcgataaagaactgttacc---tcttcataggcccttgctgctgga 419
 DB 460 agactgctctgcgataaagaactgttaccacttccctgctctttaaattggga 519
 QY 420 aaaaaacggcagaccttcgaactcttggtggtgagcttactacaataatggtgcaga 479


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FH Key Location/Qualifiers
FT 5'UTR 1..34
FT CDS 35..856
FT /tag= a
FT /tag= b
FT /product= LDL_receptor
FT 3'UTR 857..1906
FT /tag= c
FT polyA_signal 1868..1873
FT /tag= d
FT misc_feature 1889..1906
FT /tag= e
FT /note= "polyA site"
XX
XX WO617058-A1.
XX
XX PD 06-JUN-1996.
XX
XX PF 30-NOV-1995; 95WO-JP02444.
XX
XX PR 31-JUL-1995; 95JP-0214206.
XX PR 30-NOV-1994; 94JP-0321705.
XX
XX PA (NICM ) NIPPON CHEMIPHAR CO.
XX
XX PI Masaki T, Sawamura T;
XX
XX DR WPI: 1996-277778/28.
XX DR P-PSDB: AAR9857.
XX
XX PT DNA encoding denatured low-density lipoprotein receptor of mammalian
XX PT haemangioendothelial cells - useful for generating antibodies for
XX PT use in detection of LDL in biological samples
XX
XX PS Claim 1; Page 27-30; 44pp; Japanese.
XX
XX CC The present sequence is that of a bovine DNA which encodes a denature low
XX CC density lipoprotein (LDL) receptor isolated from haemangioendothelial
XX CC cells. The DNA is useful for the production of the receptor protein in
XX CC transformed hosts. Antibodies to the protein are useful in detection
XX CC and assays of LDL in biological samples.
XX
XX SQ Sequence 1906 BP; 541 A; 351 C; 355 G; 659 T; 0 other;

Query Match 38.6%; Score 287.2; DB 17; Length 1906;
Best Local Similarity 71.0%; Pred. No. 2,1e-73;
Matches 395; Conservative 0; Mismatches 158; Indels 3; Gaps 1;

QY 183 agccctgcagagagctgcgaactcttcagagagatccagagagactccaaggaagaat 242
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 289 agcccaagcgcgcagatcagaataatctgcccagagatcacagaagaactccaagaatgat 348
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 243 agacacccctcaacttgagctgaacgagaatcccaagaagcagagagctctacagaa 302
   ||| ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 349 agaaaccccttcgccacaagctgagatgagaatccaagaatactgaacttcaccgcga 408
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 303 gaatcagagactccaagaagcctgcgaagagctgcgaactttcagctcttgccaca 362
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 409 gaactggaatcccaagaagctctcgaagagcagaactatlaagctcctgtcccca 468
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 363 agactgctcgcgcataaagaactgttacc---tcttcacatgggccccttgctggga 419
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 469 agactgctcgcgcataaagaactgttaccatcttcctcctgtccttttaattggga 528
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 420 aaaaaaacgcgcagactgcgaactcttggtggtgcagagttactacaataatggtgcaga 479
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 529 aaaaaacgcgcagagactctgtcttcttgatgcccacttggaatlaataagacaga 588
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 480 tgatcgcattcatcttacaagaacttcccataccacccctccatcttgatgatgatt 539
   ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 589 tgaactggaattcatccagcaaatgatgtgccattccagttccctcttgatggtgatt 648
   ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | |

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QY 540 gcatcgagaagcctgcgaaccatggtatggagaaatggaactccttgaattica 599
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 649 gtcaatggaggaaaccacttaactcgttgcttgggaagaatgtaactccttgaagcccca 708
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 600 attccttaagaccagggcggttcttcaacgcatatcatccaagaactggtacact 659
   || ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 709 ctgtttgaattcagagagctgttcccgatgatatccttcaggagactgcatatat 768
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 660 tcaagacggagctgtgtcgcctgcgaactgtcatttcaattgattcagcatatgcagaa 719
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 769 tcaagagggaactgttcttgcctgaactgtcatttcaactgtcattcagtatatgtcaaaa 828
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 720 gaagacaatacatcttg 735
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 829 gaagcgcaatcatcttg 844
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 12
AAK88530
ID AAK88530 standard; DNA: 1921 BP.
XX
XX AAK88530;
AC
XX 10-SEP-1999 (first entry)
DT
XX
XX DE Bovine LOX-1 extracellular region/human IgG1 Fc region chimeric protein.
XX
XX KW LDL; denatured; oxidised; arteriosclerosis; hyperlipidaemia;
XX KW low density lipoprotein; receptor; detection; immunoglobulin;
XX KW fusion protein; chimeric protein; ss.
XX
XX OS Chimeric - Bos sp.
XX OS Chimeric - Homo sapiens.
XX
XX EN WO9932520-A1.
XX
XX PD 01-JUL-1999.
XX
XX PF 18-DEC-1998; 98WO-JP05744.
XX
XX PR 16-DEC-1998; 98JP-0358170.
XX PR 19-DEC-1997; 97JP-0364981.
XX PR 09-DEC-1998; 98JP-0349648.
XX
XX PA (NLSB ) JAPAN TOBACCO INC.
XX
XX PI Kakutani M, Masaki T, Sawamura T;
XX
XX DR WPI: 1999-418906/35.
XX DR P-PSDB: AAY24153.
XX
XX PT Fusion peptide for assay of oxidized LDL and for therapeutic use
XX
XX PS Claim 14; Page 98-102; 105pp; Japanese.
XX
XX CC The present invention describes a fusion peptide which consists of the
XX CC extracellular domain of a mammalian oxidized LDL (low density
XX CC lipoprotein) receptor, fused to a partial heavy chain of a mammalian
XX CC immunoglobulin containing all or part of the constant region. Oxidized
XX CC LDL is a denatured form of LDL occurring in patients having
XX CC arteriosclerosis or hyperlipidaemia, and the fusion peptide can be
XX CC used for the assay of oxidized LDL in biological samples from such
XX CC patients, for the diagnosis of the disorders. It can also be used
XX CC therapeutically for the prevention and treatment of arteriosclerosis and
XX CC hyperlipidaemia. The present sequence encodes a chimeric protein
XX CC comprising the bovine LOX-1 extracellular region and the human genomic
XX CC DNA immunoglobulin IgG1 Fc region.
XX
XX SQ Sequence 1921 BP; 479 A; 592 C; 481 G; 369 T; 0 other;

Query Match 38.6%; Score 287.2; DB 20; Length 1921;
Best Local Similarity 71.0%; Pred. No. 2,1e-73;

```

	Matches	395;	Conservative	0;	Mismatches	158;	Indels	3;	Gaps	1
QY	183	agccctgagaaagctgcacaactcttcagaggaagctccagagaaactcaaggaagaat	242							
Db	66	agcccaagcgccttatagaaaaaatctgcgccaggatctacagaaggaagactcaagaagaatgat	125							
QY	243	agacacctcaacttgaaagctgaagagaagaatccaaagagcagggagactcttcagaa	302							
Db	126	agaaacctctgcccaacaaagctgtagagaaatccaaagaataatgatgaacttcaacggca	185							
QY	303	gaatcaagaacctcaagaagccctgcagaagagctgcacaacttttcaggtctgtccaca	362							
Db	186	gaacctgatctccaaggaagtctgaagaagcgacgaactatcatcaggtctgtcccca	245							
QY	363	agactggtcttggtcgttaagaagaactgtgtac---tcttcataggtcccttggtcggga	419							
Db	246	agactggtctctgcacatgaagaagaactgttaccaatcttcccttggtctctttaaattgga	305							
QY	420	aaaaacccggcagacctgcacaactctcttggtggtgcaggtatctacaaatgaagtgycaga	479							
Db	306	aaaaagccagagaagaacgtcttgctcttggaagcccaactgtgcgaagatlaaagacacaa	365							
QY	480	tgatctgcacatctatcttcaagaacaaatctccacataccacctcccatcttgatgtgatt	539							
Db	366	tgaaactgaattcatcacagcaaatgatgttgcacattccacgtttccctcttgatgtgggt	425							
QY	540	gcattcggaagaagcctgcgcaccaacatggtcgtalggagaatggaactccttgaatttca	599							
Db	426	gtcaatgtggaagaaacccaattactctgtgcttggagaaatggtlactcttltgaagcccca	485							
QY	600	attctttaagaccagggagcgttctcttcaagtatatcatcaagaacactggtacact	659							
Db	486	cttgttttagaattcagggagactgcttcccgatgatatalcccttcagggaaacctgacataat	545							
QY	660	tcaagaacgagactggtgtctgcgtbaaactgtcatctaaattgcatccaagatatagtcagaa	719							
Db	546	tcaaaagggaactggttttctgctgaaaactgcatctttaactgattcagtatatgtcca	605							
QY	720	gaagacaataactatg 735								
Db	606	gaaggcgaaactatgt 621								

PR	02-MAR-2000; 2000JP-0057745.
PR	31-OCT-2000; 2000JP-0333116.
XX	
PA	(ABGE-) ABGENIX INC.
XX	
PI	Kobayashi Y, Tsuji H, Kamada M, Sawamura T;
XX	
DR	WPI: 2001-565503/63.
DR	P-PSDB: AAB85871.
XX	
PT	Human monoclonal antibodies recognizing oxidized low density
PT	lipoprotein receptor for treatment of atherosclerosis and
PT	cardiovascular and kidney diseases -
XX	
PS	Disclosure: Page 105-108; 131pp; Japanese.
XX	
CC	The invention provides human monoclonal antibodies and their fragments
CC	binding to human oxidized low density lipoprotein (LDL) receptor (LOX-1),
CC	and inhibiting intracellular binding of the receptor to oxidized LDL.
CC	Drug compositions containing the MAb are useful in the treatment and
CC	prevention of atherosclerosis, cardiovascular and kidney diseases,
CC	inflammatory disorders and infiltration of leukocytes. The present
CC	sequence represents an O. cuticulus LOX-1 polypeptide encoding cDNA.
XX	
XX	Sequence 1514 BP; 414 A; 375 C; 322 G; 403 T; 0 other;

Query Match	37.38;	Score 277.6;	DB 22;	Length 1514;
Best Local Similarity	70.08;	Pred. No. 1.2e-70;		
Matches 389;	Conservative 0;	Mismatches 164;	Indels 3;	Gaps 1

RESULT	13	
AAH47112		
ID	AAH47112 standard; cDNA; 1514 BP.	
XX		
AC	AAH47112;	
XX		
PT	30-NOV-2001 (first entry)	
XX		
DE	O. cuniculus LOX-1 polypeptide encoding cDNA.	
XX		
KM	LOX-1; LDL; monoclonal antibody; low density lipoprotein; human;	
KM	atherosclerosis; cardiovascular; kidney disease; inflammatory disorder;	
KM	leukocyte; ss.	
XX		
OS	Oryctolagus cuniculus.	
XX		
FH	Key	Location/Qualifiers
FT	5'UTR	1..29
FT		/*tag-- a
FT	CDS	30..866
FT		/*tag-- b
FT	3'UTR	867..1514
FT		/*tag-- c
XX		
PN	MO200164862-A1.	
XX		
XD	07-SEP-2001.	
XX		

QY	363	agactggcctcggcataagaanaacgtttcaacctt---ccatgggccccttggtcggga	419
Db	479	agactggctctgcatgnaaaacaactgttcttcgtttccctctgcatcataattatggga	538
QY	420	aaaaaacccgcagacacccttgggtggcaggtaactataccaattatgtgtgaga	479
Db	539	aagtatgcagaagagaatctgtcttcttgcgatgccagtatgttaaatacacagacaga	588
QY	480	tgaatgacattcatcttctaagaacaatttccatacacaccctcccatcttgatatggat	539
Db	599	agatctggcttcatccagaagaagacttccaatccagttcccatctcggatggatt	658
QY	540	gcattcggaagaagcctgycaccaacatggtcattgggagaatggaactccttgaattca	599
Db	659	gtctcgagaggaaccgcacactcatatgctctggaagacggtctcctctgtagccoca	718
QY	600	attctttaagaccaggggcttcttcttaagcattatcatacaagaacactgcatacct	659
Db	719	cttgttcagatccaggygtctgtttlcccaagagtaaccttccagcaccctgycataat	778
QY	660	tcaaagcggactgtgtcttgctgaanaactgcatctcaattgcatctcagcatatgcaaa	719
Db	779	acagaagggaaatgttttctgtcagacatgcatcttattgtgcatacagratctgcagaa	838
QY	720	gaagacaatatcatcttg 735	
Db	839	gaaggcaaatctgctg 854	

RESULT 14

AAL25166/c
 ID AAL25166 standard; cDNA; 540 BP.
 XX
 AC AAL25166;
 XX
 DT 07-DEC-2001 (first entry)
 XX
 DE Human breast cancer expressed polynucleotide 17623.
 XX
 KW Human; breast cancer; cell marker; cytostatic; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO200151628-A2.
 XX
 PD 19-JUL-2001.
 XX
 PF 10-JAN-2001; 2001WO-US00798.
 XX
 PR 14-JAN-2000; 2000US-0176077.
 XX
 PR 14-MAR-2000; 2000US-0189167.
 XX
 PR 24-MAR-2000; 2000US-0192099.
 XX
 PR 29-MAR-2000; 2000US-0193480.
 XX
 PR 15-MAY-2000; 2000US-0205230.
 XX
 PR 09-JUN-2000; 2000US-0211315.
 XX
 PR 25-JUL-2000; 2000US-0220534.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Lillie J, Xu Y, Wang Y, Steimann K;
 XX
 DR WPI; 2001-451856/48.
 XX
 PT New peptide useful as a marker for the diagnosis of breast cancer
 XX
 PS Claim 1; Page 3262; 3695pp; English.
 XX
 SS The invention relates to human breast cancer expressed polynucleotides
 CC (AAL07544-AAL26789) and methods of assessing whether a patient is
 CC afflicted with breast cancer by examining the correlation between the
 CC expression of certain markers and the cancerous state of breast cells.
 CC The polynucleotides and encoded polypeptides are potential markers for
 CC detecting, diagnosing, monitoring, characterizing treating and
 CC potentially preventing breast cancer. The polynucleotides and encoded
 CC polypeptides are also useful for isolating compounds with cytostatic
 CC activity.
 CC
 XX
 SQ Sequence 540 BP; 128 A; 120 C; 126 G; 166 T; 0 other;
 XX
 Query Match 27.4%; Score 203.8; DB 22; Length 540;
 Best Local Similarity 70.5%; Pred. No. 2.4e-49;
 Matches 315; Conservative 0; Mismatches 127; Indels 5; Gaps 3;
 XX
 QY 207 ttcaagagagtcceccagagagaaactcaaggaagatagacacccctacactgaagctgaa 266
 DB 447 TTCACAGAGGTCAGAAAGAAAGAAATTCAGAGAAATGATPAAAAACCTTCGCGGGAAGTGTAT 388
 QY 267 cgagagaatcccaagagcagagagcttcacagaag-aaatcagaacctccaagaagccc 325
 DB 387 TGAGAAATCCAAAGAGCAATGTGAACTTCACCCAGCAATCTGAAATCTCCAAAGAAACAT 328
 QY 326 tgcgaagagcgcgaacacttcagcttccttcacacagaagcgcgtctggcataaag-aa 384
 DB 327 TGAAGAAGAGTACCAAAATTTGTTAGCTCTGTCGCCAGAGCTGGATCTGGCATGGAGAA 268
 QY 385 aactgtactcctc---ccatgggcctttggctgggaaaaaaacccgcgcagacccgcacaa 441
 DB 267 AACCTGTACCTATTTTCCTCGGGCTCATTTAACTGGGAAAGCAAGCAAGAGGCTTG 208
 QY 442 tcttgggtggcagcttactacaataatggtcgaagatgactcagatcatccttcaaa 501
 DB 207 TCTTTGATGCCAAGTGTGCTGAAATTAATFACACAGCTGATGATCTGACTTCATCCAGCAA 148

QY 502 gcaattcccaaccaccctccattctgagatgagatgcatcggaagaagccctggccaa 561
 DB 147 GCAATTTCTTATTCACAGTTTTCATTCGATGGGGCTCTCGAGAGAACCCACACTAC 88
 QY 562 ccatggctatgggagaatggaactccttgaattcaattcatttaagaccagggcgtt 621
 DB 87 CCATGGCTCTGGAGGAGGAGGTTCTCTTGTGATGCCCACTTATTTAGAGTCCGAGCGCT 28
 QY 622 tcttacagctatcatcacaagcaac 648
 DB 27 GTCTCCAGACATPACCTTCAGGTAC 1
 RESULT 15
 ID AAA45084
 AC AAA45084 standard; cDNA; 532 BP.
 XX
 AC AAA45084;
 XX
 DT 21-AUG-2000 (first entry)
 XX
 DE Human secreted expressed sequence tag SEQ ID NO:1659.
 XX
 KW Human; mouse; chicken; rat; secreted expressed sequence tag; SEST;
 KW expressed sequence tag; EST; probe; chemotactic; proliferative;
 KW immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;
 KW thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;
 KW antiviral; antidiabetic; antiasthmatic; vulnery; antiparkinsonian;
 KW anticancer; osteoprotective; neuroprotective; nootropic; antipsoriatic;
 KW cerebroprotective; anticonvulsant; antidepressant; gene therapy;
 KW vaccine; autoimmune disorder; multiple sclerosis; allergic condition;
 KW insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
 KW lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
 KW central nervous system disorder; Alzheimer's disease; stroke;
 KW Parkinson's disease; Huntington's disease; coagulation disorder;
 KW haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
 KW tumour; infection; depression; psoriasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200021991-A1.
 XX
 PD 20-APR-2000.
 XX
 PF 15-OCT-1999; 99WO-US24206.
 XX
 PR 15-OCT-1998; 98US-0104436.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
 XX
 PT Weirberg D, Treacy M, Bowman MR;
 XX
 PS WPI; 2000-317938/27.
 XX
 DR Isolated polynucleotides, and encoded proteins, comprising secreted
 XX expressed sequence tags (seSTs), useful for treating various disorders
 XX such as autoimmune, infectious, and central nervous system disorders -
 XX
 XX Claim 1; Page 633; 803pp; English.
 XX
 CC AAA43426 to AAA45925 represent specifically claimed secreted expressed
 CC sequence tags (seSTs), isolated from human, mouse, chicken and rat
 CC tissue sources. The seSTs can have a range of activities depending on
 CC the tissues they were isolated from. The activities include:
 CC chemotactic; proliferative; immunomodulatory; haematopoietic;
 CC chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;
 CC cytostatic; antibacterial; antifungal; antiviral; antidiabetic;
 CC antiasthmatic; vulnery; anticancer; osteoprotective; neuroprotective;
 CC nootropic; antiparkinsonian; antipsoriatic; cerebroprotective;
 CC anticonvulsant; and antidepressant. The seSTs can be used for gene
 CC therapy and in vaccines. The seSTs are useful as probes for the

CC identification and isolation of full-length cDNAs and genomic DNA
 CC molecules which correspond to the SESTs. Proteins encoded by the SESTs
 CC are useful in assays for determining biological activity and raising
 CC antibodies. They may be useful for treatment of autoimmune disorders
 CC (multiple sclerosis, insulin dependent diabetes), allergic conditions
 CC (asthma), myeloid or lymphoid cell deficiencies, wounds, ulcers,
 CC osteoporosis, osteoarthritis, central nervous system disorders
 CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
 CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
 CC disease), tumours, bacterial, fungal or viral infections, depression and
 CC psoriasis. AAA45926 to AAA45931 represent linker variants which are given
 CC in the exemplification of the present invention.

xx
 SQ Sequence 532 BP; 162 A; 132 C; 127 G; 111 T; 0 other:

Query Match 21.7%; Score 161.6; DB 21; Length 532;
 Best Local Similarity 88.0%; Pred. No. 4.8e-37;
 Matches 176; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

```

QY 62 agaagcctaagaaggaggtcccaagagagaaactcaagggaagatagacacatcacccgga 121
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Db 333 aaacacttcacagaaatcaagaagaaactgaaagaaagatagacacccctcacccaga 392

QY 122 agctgagcaggaataatccaagaagcaggaagcttctgcagatgatcagaactccaag 181
   || || || || || || || || || || || || || || || || || || || || || ||
Db 393 agctgaaacgagaatccaagaagcaggaagcttctacagaagatcagaactccaag 452

QY 182 aagccctgcagagagctcgaactcttcagaggaagtcaccaagagaactcaaggaaaga 241
   || || || || || || || || || || || || || || || || || || || || || ||
Db 453 aagccctgcagaaagcctgcgaactcttcagaggaagtcaccaagagaactcaaggaaaga 512

QY 242 tagaacacctcacttgaag 261
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Db 513 tagaacaccccccacctcgaag 532
  
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Search completed: August 19, 2002, 22:01:22
 Job time: 9047 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 21:01:18 ; Search time 48.91 Seconds
(without alignments)
3736.482 Million cell updates/sec

Title: US-09-898-554-13
Perfect score: 744
Sequence: 1 atgactttgacgaagat.....caatcattgcaattag 744

Scoring table: IDENTITY_NIC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	298.2	40.1	1318	2	US-08-809-494A-5
2	298.2	40.1	1318	4	US-09-352-302-5
3	287.2	38.6	1897	2	US-08-809-494A-1
4	287.2	38.6	1897	4	US-09-352-302-1
5	287.2	38.6	1906	2	US-08-809-494A-3
6	287.2	38.6	1906	4	US-09-352-302-3
7	72.4	9.7	990	2	US-08-688-342-2
8	72.4	9.7	990	2	US-08-113-788-2
9	61.2	8.2	528	3	US-08-772-440-7
10	61.2	8.2	2298	3	US-08-772-440-1
11	59.4	8.0	7218	1	US-08-232-463-14
12	49.6	6.7	378	3	US-08-772-440-9
13	45.2	6.1	5661	3	US-08-938-105-2
14	41.8	5.6	340	1	US-08-182-175A-104
15	41.8	5.6	340	5	PCT-US92-06412-104
16	40	5.4	16442	3	US-08-781-891-208
17	39.2	5.3	1212	4	US-09-591-435-11
18	38.6	5.2	289	4	US-09-007-005-17
19	38.6	5.2	289	4	US-09-244-796-17
20	38.4	5.2	926	2	US-08-919-145-1
21	38.4	5.2	926	2	US-09-344-889-1
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27	36.6	4.9	2680	2	US-08-533-306A-5

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31	36	4.8	533	6	5482709-5
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33	35	4.7	1242	5	PCT-US93-03077-4
34	35	4.7	3279	5	PCT-US93-03077-2
35	33.8	4.5	4456	4	US-09-095-443-1
36	33.6	4.5	187	1	US-08-182-175A-90
37	33.6	4.5	187	1	US-08-474-633A-78
38	33.6	4.5	187	5	PCT-US92-06412-90
39	33.6	4.5	243	1	US-08-182-175A-56
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44	33.6	4.5	1489	4	US-09-265-566-1
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ALIGNMENTS

RESULT 1
US-08-809-494A-5
Sequence 5, Application US/08809494A
Patent No. 5962260
GENERAL INFORMATION:
APPLICANT: Sawamura, Tatsuya
TITLE OF INVENTION: Modified Low-Density Lipoprotein
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAlister Fisher Nissen Goldberg & Kiel
STREET: 261 Madison Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,494A
FILING DATE: 24-MAR-1997
CLASSIFICATION: A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-321705
FILING DATE: 30-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-214206
FILING DATE: 31-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Goldberg, Jules E.
REGISTRATION NUMBER: 24408
REFERENCE/DOCKET NUMBER: JC-YY-4363PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 986-4090
TELEFAX: 212 818-9479
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1318 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens

Sequence 5, Appli
Sequence 3, Appli
Sequence 3, Appli
Patent No. 5482709
Patent No. 5273901
Sequence 4, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 90, Appli
Sequence 78, Appli
Sequence 90, Appli
Sequence 56, Appli
Sequence 74, Appli
Sequence 56, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 13, Appli


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: Sequence 1, Application US/09352302
: Patent No. 6197937
:
: GENERAL INFORMATION:
: APPLICANT: Sawamura, Tatsuya
: APPLICANT: Masaki, Tomoo
: TITLE OF INVENTION: Modified Low-Density Lipoprotein
: TITLE OF INVENTION: Receptor
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: McAlaily Fisher Nissen Goldberg & Kiel
: STREET: 261 Madison Avenue
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10016-2391
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/352,302
: FILING DATE: 12-JUL-1999
:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-321705
: FILING DATE: 30-NOV-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 7-214206
: FILING DATE: 31-JUL-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Goldberg, Jules E
: REGISTRATION NUMBER: 24408
: REFERENCE/DOCKET NUMBER: JG-YJ-4363PCT/D
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212 986-4090
: TELEFAX: 212 818-9479
:
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1897 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Bos taurus
: TISSUE TYPE: vascular endothelial cells
: IMMEDIATE SOURCE:
: LIBRARY: Bovine aortic endothelial cell cDNA
: CLONE: pBLOX-1
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: FEATURE:
: NAME/KEY: polyA_site
: LOCATION: 1880..1897
: FEATURE:
: NAME/KEY: misc_RNA
: LOCATION: 1859..1864
: OTHER INFORMATION: /function="PolyA Signal"
: FEATURE:
: NAME/KEY: 5'UTR
: LOCATION: 1..34
: FEATURE:
: NAME/KEY: 3'UTR
: LOCATION: 848..1897
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 35..847
:
: US-09-352-302-1

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Query Match	38.68;	Score 287.2;	DB 4;	Length 18977
Best Local Similarity	71.08;	Pred. No. 1.1e-79;		

	Matches	395;	Conservative	0;	Mismatches	158;	Indels	3;	Gaps	1
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QY	480	tgatctgcattcatcttataagaasaattccatccacocctccatctcgtatggatt	539							
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QY	540	gcatcggagaagaagccctggtccaacacatctggtctatgtagaagatgnaactctctgaatttcca	599							
Db	640	GTCATGTAGAAACCAATTACTCTGGCTTTGGGAAGATGTACTCTCTTGACGCCCA	699							
QY	600	attccttaagaccaggggcgttctcttacaagctatatcatcaagaacatgtgcatacct	659							
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QY	660	tcaaatcagagactgtgtctgcgtgaaaactgtcatcttaattgcatccagcatatgtccagaa	719							
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US-08-809-494A-3										
; Sequence 3, Application US/08809494A										
; Patent No. 5962260										
; GENERAL INFORMATION:										
; APPLICANT: Sawamura, Tatsuya										
; APPLICANT: Masaki, Tomoo										
; TITLE OF INVENTION: Modified Low-Density Lipoprotein										
; TITLE OF INVENTION: Receptor										
; NUMBER OF SEQUENCES: 8										
; CORRESPONDENCE ADDRESSES:										
; ADDRESSEE: McQuay Fisher Nissen Goldberg & Kiel										
; STREET: 261 Madison Avenue										
; CITY: New York										
; STATE: NY										
; COUNTRY: USA										
; ZIP: 10016-2391										
; COMPUTER READABLE FORM:										
; MEDIUM TYPE: Floppy disk										
; COMPUTER: IBM PC compatible										
; OPERATING SYSTEM: PC-DOS/MS-DOS										
; SOFTWARE: Patentln Release #1.0, Version #1.30										
; CURRENT APPLICATION DATA:										
; APPLICATION NUMBER: US/08/809,494A										
; FILING DATE: 24-MAR-1997										
; CLASSIFICATION: 435										
; PRIOR APPLICATION DATA:										
; APPLICATION NUMBER: JP 6-321705										
; FILING DATE: 30-NOV-1994										
; PRIOR APPLICATION DATA:										


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: APPLICATION NUMBER: JP 7-214206
: FILING DATE: 31-JUL-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Goldberg, Jules E
: REGISTRATION NUMBER: 24408
: REFERENCE/DOCKET NUMBER: JG-YY-4363PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212 986-4090
: TELEFAX: 212 818-9479
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1906 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Bos taurus
: TISSUE TYPE: Vascular endothelial cells
: IMMEDIATE SOURCE:
: LIBRARY: Bovine aortic endothelial cells CDNA
: CLONE: pBLOX-1
: FEATURE:
: NAME/KEY: polyA_site
: LOCATION: 1889..1906
: FEATURE:
: NAME/KEY: misc_RNA
: LOCATION: 1864..1873
: OTHER INFORMATION: /function= "Polya Signal"
: FEATURE:
: NAME/KEY: 5'UTR
: LOCATION: 1..34
: FEATURE:
: NAME/KEY: 3'UTR
: LOCATION: 857..1906
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 35..856
: US-08-809-494A-3

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Query Match 38.6%; Score 287.2; DB 2; Length 1906;
 Best Local Similarity 71.0%; Pred. No. 1.1e-79;
 Matches 395; Conservative 0; Mismatches 158; Indels 3; Gaps 1;

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QY 133 agccctgagagagctgcgaactcttcagagagatccagagagaactcaaggaagaat 242
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DB 349 AGAAACCCCTTGCCACAAAGCTGATGAGAAATCAAGAACTAAATGGAATTCACCGCA 408
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RESULT 6
 US-09-352-302-3
 Sequence 3, Application US/09352302
 Patent No. 6197937
 GENERAL INFORMATION:
 APPLICANT: Sawamura, Tatsuya
 TITLE OF INVENTION: Modified Low-Density Lipoprotein
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 STREET: McAlay Fisher Nissen Goldberg & Kiel
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10016-2391
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/352,302
 FILING DATE: 12-JUL-1999
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 6-321705
 FILING DATE: 30-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-214206
 FILING DATE: 31-JUL-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Goldberg, Jules E
 REGISTRATION NUMBER: 24408
 REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 986-4090
 TELEFAX: 212 818-9479
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1906 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Bos taurus
 TISSUE TYPE: Vascular endothelial cells
 IMMEDIATE SOURCE:
 LIBRARY: Bovine aortic endothelial cells CDNA
 CLONE: pBLOX-1
 FEATURE:
 NAME/KEY: polyA_site
 LOCATION: 1889..1906
 FEATURE:

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; NAME/KEY: misc_RNA
; LOCATION: 1864...1873
; OTHER INFORMATION: /function="PolyA signal"
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1...34
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; LOCATION: 35..856
; US-09-352-302-3

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Query Match          38.6%; Score 287.2; DB 4; Length 1906;
Best Local Similarity 71.0%; Pred. No. 1,1e-79;
Matches 335; Conservative 0; Mismatches 158; Indels 3; Gaps 1;

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QY 183 agccctgcagagagctgcaactcttcagagagagctcccaagagaaactcaaggagaaat 242
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DB 469 AGACTGCTCTGCGATGAGAAATCTGTACCAATTTCTCTGCGCTTTTATTTGGA 528
QY 420 aaaaaacgcgcagacccgtccaactcttgggtgcccagttactaaatlaagtgacaga 479
DB 529 AAAAAGCAGAGAAACGCTTGTCTTGGATGCGCCACTTGTGAAGTTAATACACAGA 588
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RESULT 7
US-08-688-342-2
; Sequence 2, Application US/08688342
; Patent No. 5871964
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Goll, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.

```

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; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/688,342
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEO ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 990 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: MMLR1D701
; CLONE: 515847
; US-08-688-342-2

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Query Match          9.7%; Score 72.4; DB 2; Length 990;
Best Local Similarity 52.8%; Pred. No. 5,7e-13;
Matches 204; Conservative 0; Mismatches 176; Indels 6; Gaps 2;

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DB 403 TAAAGATAGACAGCTCAATGAAATTTGGGATTTAATGAAACAGTGTCTTCCAACTG 462
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RESULT 8
US-09-113-788-2
; Sequence 2, Application US/09113788
; Patent No. 5969104
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Cocks, Benjamin G.

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1      RESULT          9
2      US-08-772-440-7
3      : Sequence 7, Application US/08772440
4      : Patent No. 6046158
5      : GENERAL INFORMATION:
6      :   APPLICANT: Afilizumab, Kiyoshi
7      :   APPLICANT: Takashima, Akira
8      :   TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
9      :   TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
10     :   TITLE OF INVENTION: THEREOF
11     :   NUMBER OF SEQUENCES: 42
12     :   CORRESPONDENCE ADDRESSES:
13     :     ADDRESSEE: Arnold, White & Durkee
14     :     STREET: P.O. Box 4433
15     :     CITY: Houston
16     :     STATE: Texas
17     :     COUNTRY: USA
18     :   ZIP: 77210
19     :   COMPUTER READABLE FORM:
20     :     MEDIUM TYPE: Floppy disk
21     :     OPERATING SYSTEM: IBM PC compatible
22     :     SOFTWARE: Patentin Release #1.0, Version #1.30
23     :   CURRENT APPLICATION DATA:
24     :     APPLICATION NUMBER: US//08/772.440
25     :     FILING DATE: CONCURRENTLY HERewith
26     :     CLASSIFICATION: 435
27     :   ATTORNEY/AGENT INFORMATION:
28     :     NAME: Parker, David L.
29     :     REGISTRATION NUMBER: 32,165
30     :     REFERENCE/DOCKET NUMBER: UTXD:493
31     :     TELECOMMUNICATION INFORMATION:
32     :       TELEPHONE: 512/418-3000
33     :       TELEFAX: 512/474-7577
34     :   INFORMATION FOR SEQ ID NO: 7:
35     :     SEQUENCE CHARACTERISTICS:
36     :       LENGTH: 528 base pairs
37     :       TYPE: nucleic acid
38     :       STRANDEDNESS: single
39     :       TOPOLOGY: linear
40     :   US-08-772-440-7

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Db	455	tatgatattcactgagatcacaggtctacacaccaaattctgcatacttcttcattacagtatct	514
Oy	713	gtccagaagaa	722
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RESULT 10
US-08-772-440-1
; Sequence 1, Application US/08772440

GENERAL INFORMATION:
APPLICANT: Arizumi, Kiyoshi
APPLICANT: Takashima, Akira
TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
TITLE OF INVENTION: LECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:

ADDRESS: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA

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;  * ZIP:  77210
;  * COMPUTER READABLE FORM:
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:
: MEDIUM TYPE: Floppy disk
: COMPUTER : IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/772,440
FILING DATE: CONCURRENTLY HERewith

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Parker, David L.
REGISTRATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
EDWARD 510 440 3000

TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 2298 base pairs
TYPE: nucleic acid

```

; STRANDEDNESS: single
; TOPOLOGY: linear
;
;

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;
; FEATURE:
; NAME/KEY: modified_base
; POSITION: 1000

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; LOCATION: 1966
; OTHER INFORMATION: /mod_base- OTHER
; OTHER INFORMATION:

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OTHER INFORMATION: /note= "Y = C or Y
US-08-772-440-1

Query Match	8.2%	Score	61.2	DB	3	Length	2298
Best Local Similarity	48.2%	Pred. No.	2.7e-09				
Matches	236	Conservative	0	Mismatches	248	Indels	6
						Gaps	2

QY 239 agatagacacccctcaccttgaagctgacagagaatccaaagagcagagagcttctac 29

Db 327 AGAAGACCACTTCCTATCAGAATAAAGAGAACCAACAAGCCACAGCAATCATCTTTAG 388

QY 299 agaagaatcagaacctccagaagccctgcagaagagctgcaaaccttcaggtccctgtc 358

Db 387 ATGAGAAAGTGGCTTCCTCCAAAGGCATCCAAACTACAGAGAGTTCCTCAGTCTTGGCC 446

[illegible]

RESULT 11
US-08-232-463-14/c
; Sequence 14, Application US/08232463

; Patent No. 5670367
; GENERAL INFORMATION

```

; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
;

```

APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500

CITY: Alexan
STATE: VA

COUNTRY: USA
ZIP: 22313-0299

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy
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;
;      COMPUTER:   IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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; SOFTWARE: Patentin Release #1.0,
; CURRENT APPLICATION DATA:
;

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APPLICATION NUMBER: US/08/232,463
FILING DATE: 08/23/2008

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: US/07/935,313
FILING DATE: 07-04-2007

APPLICATION NUMBER: EP 91 114 300
FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMIGRATION

TELECOMMUNICATION INFORMATION
TELEPHONE: (703) 836-9300
TELEFAX: (703) 503-4100

TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR THE

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; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
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LENGTH: /218 base pairs
TYPE: nucleic acid
; ;

RESULT 12
 US-08-772-440-9
 Sequence 9, Application US/08772440
 Patent No. 6046158
 GENERAL INFORMATION:
 APPLICANT: Arizumi, Kiyoshi
 APPLICANT: Takashima, Akira
 TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
 TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
 TITLE OF INVENTION: THEREOF
 NUMBER OF SEQUENCES: 42
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P. O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: USA
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/772,440
 FILING DATE: CONCURRENTLY HERewith
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Parker, David L.
 REGISTRATION NUMBER: 32,165
 REFERENCE/DOCKET NUMBER: UTXD:493
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577

```

1  GENERAL INFORMATION:
2  APPLICANT: Leitwand, Leslie A.
3  APPLICANT: Vikstrom, Karen L.
4  TITLE OF INVENTION: TRANSGENIC MODEL FOR HEART FAILURE
5  NUMBER OF SEQUENCES: 3
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE: Sheridan Ross P.C.
8  STREET: 1700 Lincoln St., Suite 3500
9  CITY: Denver
10 STATE: CO
11 COUNTRY: U.S.A.
12 ZIP: 80203
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: Patent In Release #1.0, Version #1.30
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/938,105
20 FILING DATE:
21 CLASSIFICATION:
22 ATTORNEY/AGENT INFORMATION:
23 NAME: Crook, Mannell M.
24 REGISTRATION NUMBER: 31,071
25 REFERENCE/DOCKET NUMBER: 3595-4
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: (303) 863-9700
28 TELEFAX: (303) 863-0223
29 INFORMATION FOR SEQ ID NO: 2:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 5661 base pairs
32 TYPE: nucleic acid
33 STRANDEDNESS: single
34 TOPOLOGY: linear
35 MOLECULE TYPE: cDNA
36 FEATURE:
37 NAME/KEY: CDS
38 LOCATION: 1..5661
39 US-08-938-105-2

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Query Match 6.1%; Score 45.2; DB 4; Length 5661;
Best Local Similarity 46.1%; Pred. No. 0.00042;
Matches 152; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

QY 13 gacaaagtgaagctctgcaatgacgagcctgatacagaagtcatgtgcaagaacctaa 72
DB 2563 GACACACTGATCAAGAACAGATCCAGCTGAGGCCCAAGGATGAGATGACCGAGAG 2622
QY 73 gaggaagctccagagagaactcaaggagaatagacacatcccggaagctggagcg 132
DB 2623 CTGGAGACAGAGAGAGATGAACGCCGAGCTCAGCGCAAGAGCGCAAGCTGGAGAG 2682
QY 133 aatccaaagagcagagagagctctctgcatgatcacaacctccaagaagccctgcag 192
DB 2683 GAGTGTCTCAGAGCTCAAGAAAGATATGATGACCTGAGCTGACCTGGCCAGAGTGGAG 2742
QY 193 agatgtcgaactcttcagagagagctccagagagaactcaaggagaatagacacctc 252
DB 2743 AAGGAAAGCACCACAGAGAGAGGTTAAAAACCTGACAGAGAGATGCGCGGCTG 2802
QY 253 acctgaagctgagagagaatcccaagagcagagagctctacagaagaatcagaac 312
DB 2803 GACGAGATATTGCTCAAGCTGACCAAGAGAGAAAGCTTCAAGAGGCCCAACAGCAA 2862
QY 313 ctccaagaagccctgcaagaagctgcaaac 342
DB 2863 GCCCTGATGACCTTCAGGCTGAGGAAGAC 2892

RESULT 14
US-08-182-175A-104
; Sequence 104, Application US/08182175A
; Patent No. 5559223
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing F
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,175A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELE: 835420
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: ~ 340 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: E. coli
; CELL TYPE: DH5 alpha
; IMMEDIATE SOURCE:
; CLONE: segment 534 [seg 534]
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..326
; OTHER INFORMATION: /function="synthetic seed storage protein"
; OTHER INFORMATION: /product="protein"
; OTHER INFORMATION: /gene="ssp"
; OTHER INFORMATION: /standard_name="SSP-534"
; US-08-182-175A-104

Query Match 5.6%; Score 41.8; DB 1; Length 340;
Best Local Similarity 47.5%; Pred. No. 0.0011;
Matches 124; Conservative 0; Mismatches 137; Indels 0; Gaps 0;

QY 60 caagaagccctaaagagagagctccagagagaactcaaggagaatagacaccatcccg 119
DB 2 CATGGAGGAGAGATGAAAAAGCTCAAGAGGAAATGCTAAGATGAAGACGAATATG 61
QY 120 gaagctgagcgaagaatccaaagagagagctctctgcatgatcagaacctca 179
DB 62 GAACCTGAAAGAGAGAAATGAAAGCTCGAAGAGAGAGATGAAGCTATGAGAGAAAGAT 121
QY 180 agaagccctgagagagctgcaaacctcttcagagagagctccagagaagaactcaaggaaa 239
DB 122 GAAAGAGCTGGAAGAAAGATGAAAGCTATGAGAGACAAAGATGAATGCTTGAGGAAAA 181
QY 240 gatagacacctcacttgaagctgagacgagaatccaaagagcagagagagcttaca 299
DB 182 GATGAAGAGAGCTCGAAGAGAGATGAAGCTCATGAGAGAGAGATGAAGAGCTCGAAGA 241
QY 300 gaagaatcagaacctccaaga 320
DB 242 AAGATGAAGGCAATGAGAGA 262

RESULT 15
PCT-US92-06412-104
; Sequence 104, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containin
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 330
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692

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REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
TELEX: 835420
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: E. coli
CELL TYPE: DH5 alpha
IMMEDIATE SOURCE:
CLONE: segment 534 [seg 534]
FEATURE:
NAME/KEY: CDS
LOCATION: 3..326
OTHER INFORMATION:
/feature= "synthetic seed storage protein"
/product= "protein"
OTHER INFORMATION:
/gene= "ssp"
OTHER INFORMATION:
/standard_name= "SSP-534"
CCT-US92-06412-104

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Query Match	5.6%	Score 41.8	DB 5	Length 340	1
Best Local Similarity	47.5%	Pred. No. 0.0011			
Matches 124; Conservative	0	Mismatches 137		Indels 0	Gaps 0

[illegible]

Search completed: August 19, 2002, 22:02:32
Job time: 3674 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 19:03:05 ; Search time 1710.4 seconds
(without alignments)
5870.986 Million cell updates/sec

Title: US-09-898-554-13

Perfect score: 744

Sequence: 1 atgaccttgcagacaagat.....caatcattgcaaatgtag 744

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST.*
1: em_estbda.*
2: em_estbhm.*
3: em_estln.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estlo.*
8: em_hlc.*
9: gb_estl.*
10: gb_est2.*
11: gb_hlc.*
12: gb_gss.*
13: em_gss_hum.*
14: em_gss_inv.*
15: em_gss_pln.*
16: em_gss_vrt.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	297.8	40.0	851	9 AU135631	AU135631 AU135631
2	285.4	38.4	900	9 AU1546824	AU1546824 AU1546824
3	265.6	35.7	827	10 B1522607	B1522607 603175620
4	244.8	32.9	514	9 A1243883	A1243883 qh78a08.x
5	241.4	32.4	499	10 BG383949	BG383949 302408 MA
6	199.4	26.8	426	9 AA682386	AA682386 zj86b12.s
7	197.6	26.6	718	9 AU138854	AU138854 AU138854
8	197.6	26.6	760	9 AU137679	AU137679 AU137679
9	177.2	23.8	731	9 AU135523	AU135523 AU135523
10	171.6	23.1	746	10 BG547497	BG547497 602574930
11	171.6	22.7	934	9 AU151100	AU151100 AU151100
12	168.8	22.1	910	10 B1601086	B1601086 603249577
13	153.4	20.6	526	10 B1289895	B1289895 UR-R-DK0-
14	140	18.8	472	10 R62556	R62556 y11b10.r1
15	132.6	17.8	378	10 R07930	R07930 yf16e04.r1
16	116.4	15.6	480	10 B1541952	B1541952 456045 MA
17	111	14.9	780	10 BG573639	BG573639 602594660

c	18	92.4	12.4	407	10 BF934257	BF934257 IL5-MT027
c	19	82.8	11.1	258	10 BF895809	BF895809 IL2-MT017
c	20	77.8	10.5	277	9 AA620341	AA620341 af07a11.s
c	21	74.4	10.0	659	10 B1018962	B1018962 IL3-MT026
c	22	73	9.8	356	9 BB868965	BB868965 BB868965
c	23	73	9.8	363	9 BB869276	BB869276 BB869276
c	24	68.2	9.2	253	9 BB564191	BB564191 BB564191
c	25	66	8.9	320	9 BE175194	BE175194 QV2-HT057
c	26	66	8.9	673	9 AV721179	AV721179 AV721179
c	27	63	8.5	940	10 BF982378	BF982378 60230808
c	28	49	6.6	647	10 BF301405	BF301405 602029862
c	29	48.4	6.5	258	10 BF895809	BF895809 IL2-MT017
c	30	47.6	6.4	650	9 BB618338	BB618338 BB618338
c	31	45.8	6.2	644	12 A2332202	A2332202 IM0060M04
c	32	45.8	6.2	1159	12 CNS015XR	AL106041 Drosophila
c	33	45.6	6.1	294	10 BE767906	BE767906 QV1-GN006
c	34	45.4	6.1	1731	11 AK006127	AK006127 Mus muscu
c	35	45.2	6.1	567	10 BG793253	BG793253 U7SM_SM10
c	36	45.2	6.1	634	12 AZ008814	AZ008814 RPCI-23-3
c	37	44.8	6.0	486	10 BF839762	BF839762 RC3-HT010
c	38	44.8	6.0	637	10 BE395825	BE395825 601310060
c	39	44.8	6.0	865	10 BG824296	BG824296 602727315
c	40	44.8	6.0	913	10 BG120501	BG120501 602346818
c	41	44.8	6.0	1044	10 BE795516	BE795516 601590192
c	42	44.8	6.0	1123	10 BG325379	BG325379 602424064
c	43	44.6	6.0	633	10 BF127555	BF127555 601810204
c	44	44	5.9	676	10 BM095514	BM095514 fV31901.Y
c	45	44	5.9	750	10 BG120527	BG120527 602346849

ALIGNMENTS

RESULT 1
LOCUS AU135631 851 bp mRNA linear EST 24-OCT-2000
DEFINITION AU135631 PLACE1 Homo sapiens CDNA clone PLACE1002536 5', mRNA
ACCESSION AU135631
VERSION AU135631.1 GI:10996170
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 851)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.

TITLE HRI human CDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952

FEATURES
source
location/Qualifiers
1..851
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="PLACE1002536"
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/tissue_type="placenta"
/note="Vector: pME185FL3"

BASE COUNT 256 a 190 c 191 g 204 t 10 others
ORIGIN

Query Match 40.0%; Score 297.8; DB 9; Length 851;
Best Local Similarity 72.4%; Pred. No. 6; 9e-70;
Matches 399; Conservative 0; Mismatches 149; Indels 3; Gaps 1;

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QY 183 agccctgcagagagctcgaactcttcaaggaggtcccaagagaagaaactcaaggagaagat 242
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DB 81 AGCCGGCAACAGCAAGCAAGCTTCCAGAGCTCAGAAACCAACTCAAGGAATGAT 140
QY 243 agacacctcacccttgaagctgaagaaatccaaagacagaggagctctacagaa 302
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 141 AGAACCCCTTGTCGGAGCTGATGGAATCAATCAAGACCAATGCACTTCCACCA 200
QY 303 gaatcagaacctccaagaagacctcgaagagctcgaacttcaagcttcgtccaca 362
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DB 201 GAATCTGAATCTCCAAACAACTGAAAGAGTAGCAAAATTTTCACCTCTGTCGCCA 260
QY 363 agactgctcttgccataaagaactgttaccctt---ccatgggaccttggctggga 419
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DB 261 AGACTGGATCTGGCATGGAGAAACCTGTACCTATTTTCTCGGGCTCATTTTAACTGGGA 320
QY 420 aaaaacccgcagacacctcgaactcttggctggcagcttactcaaatatgttgaga 479
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 321 AAGAGCCAGAGAGAGCTGTGCTTTGGATGCCAAGTTCTGAATTTAATGACACAC 380
QY 480 tgaatcgaatcattcattcaagaacttcccaaccctcccatcttgatlgat 539
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 381 TGATCTGGACTTCATCCAGCAAGCAATTTCTATTTTCAGTTTTCATTTGATGGGGCT 440
QY 540 gactcggagaagacctggccaacatctggtatgaggaagagaaactccttgaatttca 599
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 441 GTCTCGAGAGACCCAGCTACCAATGCTCTGGAGAGAGGTTCTCTTGTGATGCCCA 500
QY 600 attcttcaagacagaggcgcttcttcttcaagctatacttcaagcaactcgttcatact 659
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 501 CTATTTTGAAGTCCGAGGCGCTGTCCTCCAGACATACCTTCAGTACCTGTCATTTAT 560
QY 660 tcaagaagagagctgtgtctgctgaagaactcgtcattcaatgcattcagaatgtcaga 719
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 561 ACACAGAGAGGCTGTATGTCGAAACATGCAATTTAGTGCCTTCAGTATATGTCAGAA 620
QY 720 gaagacaatc 730
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DB 621 GAAGGCANACC 631
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RESULT 2
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LOCUS AL546824 LTL_NFL006.PL2 Homo sapiens cDNA clone CSOD1026Y018 5
DEFINITION AL546824 LTL_NFL006.PL2 Homo sapiens cDNA clone CSOD1026Y018 5
ACCESSION AL546824
VERSION AL546824.1 GI:12880315
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 900)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1..900
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSOD1026Y018"
/clone_1lb="LTL_NFL006.PL2"
/tissue_type="placenta"

FEATURES
Source

/note="Vector: PCWVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the PCWVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 266 a 198 c 211 g 220 t 5 others
ORIGIN

Query Match 38.4%; Score 285.4; DB 9; Length 900;
Best Local Similarity 71.9%; Pred. No. 1; 6e-66;
Matches 397; Conservative 2; Mismatches 149; Indels 4; Gaps 2;

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QY 183 agccctgcagagagctcgaactcttcaaggaggtcccaagagaagaaactcaaggagaagat 242
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 245 AGCCGGCAACAGCAAGCAAGCTTCCAGAGCTCAGAAACCAACTCAAGGAATGAT 304
QY 243 agacacctcacccttgaagctgaagaaatccaaagacagaggagctctacagaa 302
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 305 AGAACCCCTTGTCGGAGCTGATGGAATCAATCAAGACCAATGCACTTCCACCA 364
QY 303 gaatcagaacctccaagaagacctcgaagagctcgaacttcaagcttcgtccaca 362
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 365 GAATCTGAATCTCCAAACAACTGAAAGAGTAGCAAAATTTTCACCTCTGTCGCCA 424
QY 363 agactgctcttgccataaagaactgttaccctt---ccatgggaccttggctggga 419
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DB 425 AGACTGGATCTGGCATGGAGAAACCTGTACCTATTTTCTCGGGCTCATTTTAACTGGGA 484
QY 420 aaaaacccgcagacacctcgaactcttggctggcagcttactcaaatatgttgaga 478
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 485 AAGAGCCAGAGAGAGCTGTGCTTTGGATGCCAATGCTGATTTATTAATGACACAG 544
QY 479 atgactcgaatcattcattcaagaacttcccaaccctcccatcttgatlgat 538
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 545 CTGATCTGAGCTTCATCCAGCAAGCAATTTCTCATTTTTCAGTATTTTTCATTTGATGGGC 604
QY 539 tgcattcgaagaagacctggccaacatctggtatgaggaagagaaactccttgaatttcc 558
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 605 TGCTCTGGAGAGAACCCAGCTACCAATGCTCTGGAGAGAGGTTCTCTTGTGATGCCCA 664
QY 599 aattcttgaagacagaggcgcttcttcttcaagctatacttcaagcaactcgttcatact 658
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DB 665 ACTTATTTAGAGTCCGAGGCGCTGCTCCAGACATACCTTCAGAGTACCTGTCATATA 724
QY 659 ttcagaagagagctgtgtctgctgaagaactcgtcattcaatgcattcagaatgtcaga 718
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 725 TACACAGAGAGAGCTGTATGTCGAAACATGCAATTTAGTGCCTTCAGTATATGTCAGA 784
QY 719 agaagacaatc 730
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DB 785 AGAAGGCANACC 796
```

RESULT 3
BI522607 827 bp mRNA linear EST 29-AUG-2001
LOCUS BI522607 603175620F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240092 5',
DEFINITION BI522607
ACCESSION BI522607
VERSION BI522607.1 GI:15347399
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 827)
NIH-MGC http://mgi.mcl.nih.gov/.

REFERENCE
AUTHORS

Db 330 GTCTTGTCTTTGGATGCGCAAGTTCTCTGAAAATTAATAGCACAGCTGATCTGTGACTCAT 271

Qy cttaacaagaacatttcccatacaacctcccatttcggaattggaattgcaatcggaagaagcc 554

Db 270 CCAGCAACACATTTTCTTACTCCAGTTTTCATTTTCGATTCGGATGGGGCTGTCTCGAGGAAACC 211

Qy 555 tggccaacacatgactaagggaagaaatgaaacttcctttgaaatttcaaatttccttaagaacag 614

Db 210 CAGCTACCCATGGCTCTGTGGAGAGAGGTCTCTCTTTGATGCCCCCTTAATTTAGAGTCCG 151

Qy 615 gggcgcttcttcaatagcatalatcaacaagaacatgcatcaactcaagaagcagcgt 674

Db 150 AGGCGCTGTCTCCGAGACATACCCCTTCAGGTACCTGTGCATATATACAACGAGGAGCTGT 91

Qy 675 gttagcgtgaanaacgcatctcaattgcatlgtcaagatalgtcaagaagaagaacaatc 730

Db 90 TTATATCGGAAATACGATTTTATAGCTGCTTCAGTATATGTCTGAGAAGGAAACACC 35

RESULT	5	499 bp	mRNA	linear	EST 12-MAR-2001
LOCUS	BC383949				
DEFINITION	BC383949				
ACCESSION	302408	MARC	1P1G	Sus scrofa	CDNA 5', mRNA sequence.
VERSION	BC383949				
KEYWORDS	BC383949.1				GI:13308421
SOURCE	EST.				
ORGANISM	p19.				
	Sus scrofa				

REFERENCE
AUTHORS
1. (bases 1 to 499)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,

TITLE	Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
JOURNAL	Unpublished (2000)
COMMENT	Contact: Smith TPL

PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smilthe@mail.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCATGATGACCAT
BACKWARD: GTTTCCAGTCACGCG
Plate: 89 row: E column: 13
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
1..499
source

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BASE COUNT      146 a      123 c      114 g      116 t
ORIGIN
/notes=Vector: PCMV SPORTR6; Site_1: XbaI; Site_2: XhoI;
library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."

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	Best Local Similarity	71.3%	Pred. No. 1,1e-54		
	Matches 333	Conservative 0	Mismatches 111	Indels 3	Gaps 1
Oy	199	gcaaacctcttagagagagctccagagagaaactcaaggaagaatagacaccctcacttg	258		
Db	33	GAATAAATTTTCTCCAGGAGATCCAAAGGGAACATCCAGATAAAGATGAAATCTTTGCCAC	92		

QY	259	aagctgaacgagaaatcccaagaagagagagcttcacagaagaacaaactccaa	318
Db	93	AAATTGGATTGAAAAATCCAGAAACTGATGGAGCTTCACAGCAGAACTTGATTTTCAA	152
QY	319	gaagccctgcacaaagaagctgtcaaaactttcagtgctcttgccacaagaactgtgctgcgat	378
Db	153	AAAGCTCTGGAGAAAGCGCAAACTTTTCAGTGCTTGGTCCCAAGACTGGGCTGGCAT	212
QY	379	aaagaanaactgttac---ctcttccatgaggcccttggctcgtgggaaaaaaacgcgcagacc	435
Db	213	GAAGAAAACTCTTACAAATTTTCTCTGCGCCACTTTACTTGGGAAAAAAGCGGGAGAAC	272
QY	436	tgccaactcttgggggtgcgcagttactacaataatgctgacagatcgtacatcacc	495
Db	273	TGCTTTGCTTTTGGATGGCCCAACTGCTGAAGATTAAATACACAGACGATCTGGAATTCATC	332
QY	496	ttacaagaacatttcccatcacacactcccatcttgcatttgcattgcacatgcgaagaagact	555
Db	333	CAGCAAACTCATGCGCCCAATTCCAGTTTCCCAATTTCTGGATGGGGTTATCTGTAGGAAACC	392
QY	556	ggccaacacatggtctatgggagaaatgaaactcccttgaatttcaattccttaagaacag	615
Db	393	AACAACATCATGGCTCTGGGAGAGCGGTACTGCTTTGAATGCCCACTGTTTAGACTCCAG	452
QY	616	ggcgcttcttaacagctatctatccacaagaagctgtgatactcca	662
Db	453	GGAGCTGCTTCCCAATGTATCTTTCAGACACTGTGGTATATACA	499

RESULT	6
AA682386/c	
LOCUS	
DEFINITION	426 bp mRNA linear EST 19-DEC-1997
	Z186b12.s1 Soares fetal_liver spleen 1MFS.S1 Homo sapiens cDNA
	clone IMAGE:461259.3' similar to SW.NKGD_HUMAN P26718 NKGD2-D type
	II INTEGRAL MEMBRANE PROTEIN ;? RNA sequence.

SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE	TITLE	JOURNAL	COMMENT
1 (bases 1 to 426)			
Hallier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Matlin, J., Moore, B., Schellenberg, K., Stepto, M., Tan, F., Theising, B., White, Y., Wyile, T., Waterston, R. and Wilson, R.	WashU-NCI human EST Project	Unpublished (1997)	Contact: Wilson RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNC ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -40ml3 fwd. EF from Amersham
High quality sequence stop: 381.
Location/Qualifiers
1. .426

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/c/clone_1lb="Soares_fetal_liver_spleen_1MFLS_S1"
//sex="male"
/dev_stage="20 week post conception fetus"
/1lb_host="DH10B (ampicillin resistant)"
//note="Organ: Liver and Spleen; Vector: pT773D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subcloned version of the original Soares fetal

```

Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel.: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomicehri.co.jp
HRI human CDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo,¹ and

RESULT	8
Locus	AU137679
DEFINITION	AU137679 760 bp mRNA linear EST 25-OCT-2000
ACCESSION	AU137679
VERSION	AU137679
KEYWORDS	AU137679.1 GI:1099200
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 760) Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yanamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.
TITLE	HRI human cDNA project
JOURNAL	Unpublished (2000)
COMMENT	Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel.: 81-438-52-3951 Fax: 81-438-52-3952 Email: genomics@hri.co.jp HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix Research Institute; cDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
FEATURES	Location/Qualifiers 1..760
source	

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/clone="PLACE1006968"					
/clone_1b="PLACE1"					
/tissue_type="placenta"					
/note="vector: pMC185FL3"					

Query Match	26.68%	Score 197.6	DB 9	Length 760
Best Local Similarity	73.48%	Pred. No. 9e-43		
Matches 292	Conservative	0	Mismatches 101	Indels 5
				Gaps 3

QY	183	agccctgcagagagctctgcaaacctctccagagagctcccgagagaaactcaagggaaagt	242
Db	313	AGCCCGGCACACAGACGAAAGAGCTTCCACAGAGTCCAGAAAACGAATCTAAGGAATGAT	372
QY	243	agacacccctcaccttgaagctgtaacgagagaaatccaaagagcagagagagacttctacaga	302
Db	373	AGAAACCTTGCTCGGAGAGCTGATGAGAAATCCAAAGACGAATGGAATCTTACCACACA	432
QY	303	gaatcagaagactccaagaagccctgcagaaagagctgcaaaactttagctcttcttcaca	362
Db	433	GAATTCGATCTCCACAAAGAACACTGACAGAGATACCAATTTCCAGCTCCTTGTCCGCA	492
QY	363	agactgctctctgcagctaaagaaactgttaactctt---ccaatggcccttggcttgga	419
Db	493	AGACTGGATCTGCGCATGCGAATACTGTTAACTTATTTTCTCGGGCTCATTTAACTGGGA	552
QY	420	aaaaaacccgacagacctgcacaaactcttggctggctgagctactactacaatlaatgctgcga	479
Db	553	AAAGAGCCACAGAGAGTGGTTGCTTTGGATGCCAAGTTGCTGAAATAATATAGCACAGC	612
QY	480	tgatctgacatcatcttacaagaacttccatacc--acctcccactctggaattgat	538
Db	613	TGATCTGGACTTCATCCACGACGAATTTCCATTCCCAAGTTTTCATTTCTGATGGAGGGCC	672
QY	539	tg-catgcgaaagacctgcgcacaccactgctcatgga	575
Db	673	TGCTCTCGGAGCAAMCCAGATTACCCATAGGCTCTTGGA	710

RESULT	9
AU135523	
LOCUS	AU135523 731 bp mRNA linear EST 24-OCT-2000
DEFINITION	AU135523 PLACE1 Homo sapiens cDNA clone PLACE1002267 5', RNA sequence.
ACCESSION	AU135523
VERSION	AU135523.1 GI:10996062
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 731) Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.
TITLE	HRI human cDNA project
JOURNAL	Unpublished (2000)
COMMENT	Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3951 Fax: 81-438-52-3952 Email: genomics@helix.co.jp HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix Research Institute; cDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute. Location/Qualifiers
FEATURES	

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/db_xref="taxon:9606"
/clone="PLACE1002267"
/clone_1b="PLACE1"
/rnause_type="placenta"
/vector="pME185FL3"
BASE COUNT
219 a 162 c 174 g 171 t 5 others
ORIGIN

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Query Match	23.8%	Score 177.2	DB 9	Length 731
Best Local Similarity	74.0%	Pred. No. 3e-37		
Matches 251, Conservative	0	Mismatches 84	Indels 4	Gaps 2

OY	183	agcccttcgaggagtctgcacactctcgaaggagtcgccgaagaagcatcaagggaagt	242
Db	313	AGCCCGGCACACAGAAGAAAGCTTCAACGAGTCAGAAAACGAATCACAAGAAATGAT	372
OY	243	agacaacctcaccttgaagcttgacgcagagaatctcaagaagcgaggagctctacaga	302
Db	373	AGAAACCCCTGTCTCGGAAGCTGAAAGAGCAAACGAAGCAAAATGGAACTTCACACCACA	432
OY	303	gaatcagaacctccaagaagccctgcgaagaagctgaacactttcaagctctgtccaca	362
Db	433	GAATTGAAATGCCAAGAACAAGTAGAGAGTAAGAACAAATTTGTCAGCTCCTTGTCGCA	492
OY	363	agact-gagctctggcataaaagaacgtttaacctt---ccatggccccttggcttgg	418
Db	493	AGACTGGGATCTGGCATGGAGAAACCTGTACTCTATTTCCTCGGGGCTCATTTAACTGGG	552
OY	419	aaaaaacccggcagacccttgcacactcttggctggcgagcttaataaattaaatggtcag	478
Db	553	AAAAAGCCCAAGAGAAGTGCTGTCTTTGGAGCCCAAGTCTGTGAATAATTAATAGCACAG	612
OY	479	atgatctgaacattcatcttaacaagaattccccatccae	517
Db	613	CTGATCTGGACTTCAATCCACACAGAATTTCTTANTCCA	651

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RESULT 10
BG547497
LOCUS
DEFINITION BG547497 746 bp mRNA linear EST 04-APR-2001
602574930F1 NIH_MGC_77 Homo sapiens CDNA clone IMAGE:4702998 5',
RNA sequence.
ACCESSION BG547497
VERSION BG547497.1 GI:13546162
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 746)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ClONTECH Laboratories, Inc.
CDNA Library Preparation: ClONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://Image.lnl.gov
Plate: L10CM1540 row: 1 column: 07
High quality sequence stop: 741.
Location/Qualifiers
1..746
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4702998"
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FEATURES
source

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us-09-898-554-13.rst

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/tissue_type="placenta"
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enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by

```

Life Technologies. Contact : Feng Liang Life Technology
a division of Invitrogen 9800 Medical Center Drive

BASE COUNT	http://fulllength.invtrogen.com"									
ORIGIN	285	a	196	c	214	g	237	t	2	others

Query Match	23.1%	Score 171.6;	DB 9;	Length 934;
Best Local Similarity	74.4%;	Pred. No. 1.1e-35;		
Matches 229; Conservative	1;	Mismatches 75;	Indels 3;	Gaps 1;

Oy 183 agccctcagagagactgtccaactcttcaggagagtcccgagagaactcaagggaaagt 242
||||| ||| |||| | |||| | |||| | |||| | |||| | ||||
Db 288 AGCCCGCAGACAGCAAGCAAGCTTCACAGSAGTCCAGAAACGAAACTCAGAGGAATGAT 347

303 gaatcaagaacctccaagaagcccttcyaagaagctcyaacatttcaagtctctgttcaca 362

D_b 408 GAATTCGAATTCCACAGAAACACTAAGAGAGTACCAAAATTTTCAGCTCCTTGTCGCGA 467
Q_y 363 agactgctcfcgcgtaaagaanaactgttacctct---ccatggccctttgctcgga 419
||||||| ||||||| ||||||| ||| | || ||||| |||||

QY 420 aaaaacgcgacagactgccaaattcttggtggcagttacctacaatlaagtgcaga 479
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 528 AAAGGCCAAGAAGACTCTTGTCTTTGGATGCCAAAGTGTCGAATAATTATGACACC 587

Oy	480	tgatcctga	487
Db	588	TGATCTGA	595

LOCUS	DEFINITION	910 bp	mrna	linear	EST 07-SEP-2001
B1601086	603249577F1 NIH.MGC.96 Homo sapiens cDNA clone IMAGE:5301234 5',				

ACCESSION [BIF601086](#)
VERSION [BIF601086.1](#) GI:15494025
KEYWORDS EST.
SOURCE human.

CONTRIBUTORS Home Department
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini, Homnidae; Homo.
REFERENCE 1 (bases 1 to 910)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

RESEARCH, HISTORY OF MEDICINE, PHARMACY AND SCIENCE COLLECTION (HMC)
UNPUBLISHED (1999)
JOURNAL
2003
COMMENT
Contact: Robert Strusberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

Genetic library preparation: Alexander O. Mironovskii (mironov@uconn.edu), Toshiyuki and Piero Carninci (RIKEN), cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL), DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MCC clone distribution information can be

	Best Local Similarity	69.1%	Pred. No.	3e-27:	
	Matches	233;	Conservative	0;	Mismatches 100; Indels 5; Gaps 3;
OY	343	tttcaagtcctcgtccacaagaactgctcctgcgaataaagaacgttaccctt---c	399		
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OY	400	cattggccccttgctcgaggaaaaaaacccgcagacacctgcacatctttggtggccaagtta	459		
Db	61	TCGGGCTCATATTAACTGGGAAAAGGCCAAGAGAGTCTTGTCTTTTGATGCCAAGTTG	120		
OY	460	ctacaatltaatggtgcsgatgatcatcattcatctcataagaattccatcacccc	519		
Db	121	CTGAATAATTATATAGACAGCTGCATGTGCATCTTCATCCAGCAACAATTTCCATTCCAGT	180		
OY	520	tccccattcgtatgtgatcgtcgcacgaagaagcctgtgccaacat-ggcataaggagaa	578		
Db	181	TTTTCCATCTCTGAGTAGGGGCTGTCTGGGAGAACCCACCCTCACCCATGGGCTGTGGAGAGA	240		
OY	579	tggaaaccttgatatttcattcaattcttta-agaccaggaggcgtctcttcataagcatatt	637		
Db	241	CGGTTCCTCTTTGATGCCCCACTTATTTAGATGATCCGAGGGCGCTCTCCACAGCATACC	300		
OY	638	catcaagaacaactgctcacacccttcaagaacggagctgltt	677		
Db	301	CTTCAGTACCTGTGCATATATTAACAAGAGGAGACTGTT	340		
RESULT	15				
LOCUS	R07930	378 bp	mRNA	linear	EST 05-APR-1995
DEFINITION	y1f6e4.1 Soares fetal liver spleen INFLS Homo sapiens CDNA clone				
ACCESSION	R07930	IMAGE:127038	5'		mRNA sequence.
VERSION	R07930.1	GI:759853			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 378)				
AUTHORS	Hallier,L., Clark,N., Dubouque,T., Elliston,K., Hawkins,M., Holman 'M., Hulman,M., Kucabst,T., Le,M., Lennon,G., Maira,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaaskis,E., Waterston , R., Williamson,A., Wohlmann,P. and Wilson,R. The Washu-Merck EST Project Unpublished (1995) Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Insert Size: 617				
TITLE	JOURNAL				
COMMENT					
FEATURES					
SOURCE					
	Location/Qualifiers				
	1..378				
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	/sex="male"				
	/dex_stage="20 week post conception fetus"				
	/lab_host="DH10B (ampicillin resistant)"				
	/note="Organ: Liver and Spleen; Vector: pTF73D (Pharmacia) with a modified polylinker; Site.1: Pac I; Site.2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer"				

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 21:57:38 ; Search time 60.72 Seconds

(without alignments)
451.832 Million cell updates/sec

Title: US-09-898-554-14

Perfect score: 1319

Sequence: 1 MTFDDMKMPANDEPQKSCG.....ENCILIAFSICQKTNHLAI 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_032802.*

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21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	972	73.7	364	22 AAB85873
2	643	48.4	278	22 AAB85871
3	639	48.4	274	22 AAB85872
4	637	48.3	273	17 AAB85872
5	637	48.3	273	17 AAB85872
6	635	48.1	273	20 AAB85869
7	596	45.2	270	17 AAB85866
8	596	45.2	270	20 AAB85866
9	594.5	45.1	273	17 AAB85870
10	582	44.1	273	17 AAB85870
11			20	AAV24153

12	258	19.6	247	20	AAV27448	Human SDCMP4 polyp
13	258	19.6	247	20	AAV73889	Human DC3 protein
14	251	19.0	201	19	AAV52837	Human C-type lectin
15	251	19.0	201	20	AAV27449	Human SDCMP4 short
16	251	19.0	201	20	AAV41764	Human DC3 protein
17	251	19.0	201	21	AAV3888	Human DC3 protein
18	251	19.0	201	21	AAV43320	Human PRO1082 (UNO
19	251	19.0	201	22	AAU29077	Human PRO polypept
20	241	18.3	281	22	AAE11943	Human PRO polypept
21	241	18.3	288	22	AAE11926	Human CG27 (or C86
22	241	18.3	307	22	AAE11939	Human CG27 (or C86
23	241	18.3	314	22	AAE11933	Human CG27 (or C86
24	231.5	17.6	180	19	AAV69236	Mouse dectn-1 His
25	231	17.5	176	19	AAV63012	Mouse dectn-1 ext
26	231	17.5	244	19	AAV63009	Mouse dectn-1. M
27	223	16.9	404	21	AAV19714	Dendritic cell spe
28	223	16.9	404	21	AAV28614	Human C-type lecti
29	223	16.9	404	22	AAV79086	Human DC-SIGN, a d
30	221	16.8	247	22	AAE11934	Human CG27 (or C86
31	221	16.8	280	20	AAV05317	Human secreted pro
32	221	16.8	280	21	AAV42619	Human ORFX ORF2383
33	221	16.8	280	21	AAV66728	Membrane-bound pro
34	221	16.8	280	22	AAE11932	Human CG27 (or C86
35	221	16.8	280	22	AAE11938	Human lipid metabo
36	221	16.8	280	22	AAU29324	Human PRO polypept
37	221	16.8	280	22	AAV93544	Human polypeptide,
38	221	16.8	280	22	AAU12400	Human PRO1131 poly
39	221	16.8	280	22	AAV65251	Human PRO1131 (UNO
40	221	16.8	280	22	AAV50959	Human PRO1131 prot
41	221	16.8	284	20	AAV31622	Human oxidised LDL
42	214	16.2	199	19	AAV63016	Mouse dectn-1 iso
43	212	16.1	404	14	AAV32188	Sequence of a non-
44	207	15.7	126	19	AAV63013	Mouse dectn-1 car
45	195.5	14.8	229	22	AAU02496	Murine secreted pr

ALIGNMENTS

```

RESULT 1
AAB85873 standard; Protein; 364 AA.
ID AAB85873;
AC AAB85873;
DE 30-NOV-2001 (first entry)
DT xx
XX Rat LOX-1 polypeptide.
DE xx
XX LOX-1; LDL; monoclonal antibody; low density lipoprotein; human;
KW atherosclerosis; cardiovascular; kidney disease; inflammatory disorder;
KM leucocyte; rat.
OS Rattus norvegicus.
PN W0200164862-A1.
PD 07-SEP-2001.
PP 02-MAR-2001; 2001WO-JP01636.
PR 02-MAR-2000; 2000JP-0057745.
PR 31-OCT-2000; 2000JP-0333116.
PA (ABGE-) ABGENIX INC.
PI Kobayashi Y, Tsuji H, Kamada M, Sawamura T;
DR WPI; 2001-565503/63.
XX N-PSDB; AAH47114.
XX Human monoclonal antibodies recognizing oxidized low density
PT lipoprotein receptor for treatment of atherosclerosis and

```

[illegible]

PA	(ABGE--)	ABGENIX INC.	
XX			
PI	Kobayashi Y, Tsuji H, Kanada M, Sawamura T;		
XX			
DR	WPI; 2001-565503/63.		
XX			
DR	N-PSDB; AAH47112.		
XX			
PS	Human monoclonal antibodies recognizing oxidized low density		
PT	lipoprotein receptor for treatment of atherosclerosis and		
PT	cardiovascular and kidney diseases		
XX			
PS	Disclosure; Page 105-108; 131pp; Japanese.		
XX			
CC	The invention provides human monoclonal antibodies and their fragments		
CC	binding to human oxidized low density lipoprotein (LDL) receptor (LOX-1),		
CC	and inhibiting intracellular binding of the receptor to oxidized LDL.		
CC	Drug compositions containing the MAb are useful in the treatment and		
CC	prevention of atherosclerosis, cardiovascular and kidney diseases,		
CC	inflammatory disorders and infiltration of leukocytes. The present		
CC	sequence represents an O. cuniculus LOX-1 polypeptide.		
XX			
SO	Sequence 278 AA;		
	Query Match	48.7%; Score 643; DB 22; Length 278;	
	Best Local Similarity	49.3%; Pred. No. 5.6e-46;	
	Matches 135; Conservative 39; Mismatches 70; Indels 30; Gaps		6;
QY	1 MTFDD-KKKRPNDEPDOKSCGKKPKKEESORELK-----GKIDTTR--- 40		
DB	5 mavddlkxrkpmkdqpdqksngkkrx--glrlfsspcwcpaavalyiclsimtlilmgm 62		
QY	41 --KIDKSKSQDEELQMIQNLQEQ---ALQRAANSSEESORELGKIDTTLTKLNESK 93		
DB	63 qllygsdillkgqanllqgenlllegvylaqqeaaasqesqelkemtletakridesk 122		
QY	94 EQEELQKNQNLQELQRAANFSGRCPODMLNKKNCYLF-HGPRGWEKNROTQOSLGQ 152		
DB	123 kqmelnhbyllhqealkrmndfispcedwlvhgrkcyllfssgsfnwessqekclsldaq 182		
QY	153 LLOIIGADDLFFILQAIHTTSPFWIGLHRRKKPGQPMLENTPLNFOFFKRGVSLQY 212		
DB	183 llklnstedlglfigatshsfpmjglsrrtkpdyawlwedgsplmhlfrtfgavsqry 242		
QY	213 SSSNCAYLQDGAVFQENCILIAFSICQKKYTNLQ 246		
DB	243 psytcaaylqkgnvfqaencilwayslqkkanllr 276		
	RESULT 3		
	AAB85872		
	ID AAB85872 standard; Protein; 274 AA.		
	AC AAB85872;		
XX			
DT	30-NOV-2001 (first entry)		
XX			
DE	S. scrofa LOX-1 polypeptide.		
XX			
KW	LOX-1; LDL; monoclonal antibody; low density lipoprotein; human;		
KW	atherosclerosis; cardiovascular; kidney disease; inflammatory disorder;		
KX	leukocyte.		
XX			
OS	Sus scrofa.		
XX			
PN	WO200164862-A1.		
XX			
PD	07-SEP-2001.		
XX			
PD	02-MAR-2001; 2001WO-JP01636.		
XX			
XX	02-MAR-2000; 2000JP-0057745.		
RR	31-OCT-2000; 2000JP-0333116.		

XX (ABGE-) ABGENIX INC.
 PA Kobayashi Y, Tsuji H, Kamada M, Sawamura T;
 XX WPI; 2001-565503/63.
 DR N-PSDB; AAA47113.
 XX
 PT Human monoclonal antibodies recognizing oxidized low density
 PT lipoprotein receptor for treatment of atherosclerosis and
 PT cardiovascular and kidney diseases
 XX
 PS Disclosure; Page 111-115; 131pp; Japanese.
 XX
 CC The invention provides human monoclonal antibodies and their fragments
 CC binding to human oxidized low density lipoprotein (LDL) receptor (LOX-1),
 CC and inhibiting intracellular binding of the receptor to oxidized LDL.
 CC Drug compositions containing the Mab are useful in the treatment of
 CC prevention of atherosclerosis, cardiovascular and kidney diseases,
 CC inflammatory disorders and infiltration of leukocytes. The present
 CC sequence represents a S. scrofa LOX-1 polypeptide.
 XX
 SQ Sequence 274 AA;

Query Match 48.4%; Score 639; DB 22; Length 274;
 Best Local Similarity 47.3%; Pred. No. 1.2e-45;
 Matches 131; Conservative 37; Mismatches 73; Indels 36; Gaps 5;

QY 1 MTFDD-KMKRANDEPDOKSCGKPKRESORELK-----GKIDIT-- 32
 Db 1 mtfddiksmkmdqpdksng--dkaegprslslrwrpaalllgllclglvltvllll 58
 QY 33 --GKIDITRKLDKSKROEELQMIQNLQALQRAANSSESORELKGTIDTLTKINE 90
 Db 59 qlsvsdllyqkvklthgedil--egqalaqqaeksqesqreltemetlahkide 115
 QY 91 KSKOEELLOKNQNLQALQRAANSFGPCPODWLHKENCYLF-HGPGWEKNROTCOSL 149
 Db 116 ksklmeqlqgnlnlqelalekaanfsgpcpqrwlwheencykfssgptswkxstencisl 175
 QY 150 GGQLQINGADDLFTILQALSHHTSPFWIGLHRRKPGOPWLMENGTPLNFOFFKTRGVSL 209
 Db 176 daqlilkinstadlfdiqalshstfpmwglstrpmswlmwedgplmpnlfrivrgavs 235
 QY 210 QLYSSNCAYLQDGAFAENCILIAFSICOKKTNHLQ 246
 Db 236 qmypsqtcaylhrgivtaencilaafsicqkranllr 272

RESULT 4
 ID AAR9588 standard; Protein; 273 AA.
 AC AAR9588;

DT 29-OCT-1996 (first entry)

DE Low density lipoprotein receptor.

KW LDL; low density lipoprotein; receptor; bovine; assay; detection;
 KW recombinant production; haemangioendothelial cell.

OS Homo sapiens.

PN WO9617058-A1.

PD 06-JUN-1996.

PF 30-NOV-1995; 95WO-JP02444.

PR 31-JUL-1995; 95JP-0214206.
 PR 30-NOV-1994; 94JP-0321705.

XX (NIMC) NIPPON CHEMIPHAR CO.
 PA Masaki T, Sawamura T;
 XX WPI; 1996-277778/28.
 DR N-PSDB; AAT32578.
 XX
 PT DNA encoding denatured low-density lipoprotein receptor of mammalian
 PT haemangioendothelial cells - useful for generating antibodies for
 PT use in detection of LDL in biological samples
 XX
 PS Claim 1; Page 31-34; 44pp; Japanese.
 XX
 CC The present sequence is that of a human denatured low density
 CC lipoprotein (LDL) receptor encoded by DNA isolated from
 CC haemangioendothelial cells. The DNA is useful for the production of
 CC the receptor protein in transformed hosts. Antibodies to the protein
 CC are useful in detection and assays of LDL in biological samples.
 XX
 SQ Sequence 273 AA;

Query Match 48.3%; Score 637; DB 17; Length 273;
 Best Local Similarity 48.9%; Pred. No. 1.8e-45;
 Matches 134; Conservative 35; Mismatches 69; Indels 36; Gaps 6;

QY 1 MTFDD-KMKRANDEPDOKSCGKPKRESORELK-----GKIDIT-- 38
 Db 1 mtfddikqlyvkddqpdksngkkak----gqlfyspwwclaaatlglvltvltmv 55
 QY 39 -----TRKLDKSKROEELQMIQNLQALQRAANSSESORELKGTIDTLTKINE 90
 Db 56 lymqslsqsdlitqganltngkklegqisargaaesgeseneletlarline 115
 QY 91 KSKOEELLOKNQNLQALQRAANSFGPCPODWLHKENCYLF-HGPGWEKNROTCOSL 149
 Db 116 kskemeqlhqnlnlqelklrvancapcpqrwlwheencylfssgfnwksgeklsl 175
 QY 150 GGQLQINGADDLFTILQALSHHTSPFWIGLHRRKPGOPWLMENGTPLNFOFFKTRGVSL 209
 Db 176 daklilkinstadlfdiqalshstfpmwglstrpmswlmwedgplmpnlfrivrgavs 235
 QY 210 QLYSSNCAYLQDGAFAENCILIAFSICOKKTN 243
 Db 236 qlypsqtcaylqrgavyaencilaafsicqkkan 269

RESULT 5
 ID AAB85869 standard; Protein; 273 AA.
 AC AAB85869;

DT 30-NOV-2001 (first entry)

DE Human LOX-1 polypeptide.

KW LOX-1; LDL; monoclonal antibody; low density lipoprotein; human;
 KW atherosclerosis; cardiovascular; kidney disease; inflammatory disorder;
 KW leukocyte.

OS Homo sapiens.

PN WO200164862-A1.

PD 07-SEP-2001.

PF 02-MAR-2001; 2001WO-JP01636.

PR 02-MAR-2000; 2000JP-0057745.
 PR 31-OCT-2000; 2000JP-0333116.

PA (ABGE-) ABGENIX INC.
 XX Kobayashi Y, Tsuji H, Kamada M, Sawamura T;
 XX MPI: 2001-565503/63.
 DR N-PSDB; AAA47105.
 XX
 XX Human monoclonal antibodies recognizing oxidized low density
 PT lipoprotein receptor for treatment of atherosclerosis and
 PT cardiovascular and kidney diseases
 XX
 PS Disclosure: Page 87-92; 131pp; Japanese.
 XX
 CC The invention provides human monoclonal antibodies and their fragments
 CC binding to human oxidized low density lipoprotein (LDL) receptor (LDX-1),
 CC and inhibiting intracellular binding of the receptor to oxidized LDL.
 CC Drug compositions containing the Mab are useful in the treatment and
 CC prevention of atherosclerosis, cardiovascular and kidney diseases,
 CC inflammatory disorders and infiltration of leukocytes. The present
 CC sequence represents a human LDX-1 polypeptide.
 XX
 CC Sequence 273 AA:

Query Match 48.3%; Score 637; DB 22; Length 273;
 Best Local Similarity 48.9%; Pred. No. 1.8e-45;
 Matches 134; Conservative 35; Mismatches 69; Indels 36; Gaps 6;

QY 1 MTFDD-KMKPANDPPDKSGKKPKESORELK-----GKIDT-- 38
 DB 1 mtfddkikgtvkdpqeksnqkka-----gldflyspwlaaatlgvclgvlvltlmv 55
 QY 39 -----TRKLDEKSKQEDELQMIQNLQ---EALQRAANSSEESORELKIDITLTKLNE 90
 DB 56 lmqqlsqvsdlltqeganltqkkllegqtsarqaeasqesenelekmetarkline 115
 QY 91 KSKQEDELQKQNLQALQRAANFSGPCQDMLMKENCYLF-HGPFGEKRNQTCQSL 149
 DB 116 ksqegmelhqnlnlqetlkrvancsapcpqdwlmhngencyltsqsfmweksqekcls1 175
 QY 150 GGQLQINGADDLFTILQAISSHSTSPFWIGLHRRKKGQPLWENGTPPLNFQFRTGVS 209
 DB 176 dakllkinstadldlfgqatsysfpmglstrnpsypwlvwedgspjlmphlfrvgavs 235
 QY 210 QLYSSNCAYLDGAVFAENCILIASFCOKTN 243
 DB 236 qlypsgtcaylgrgavyaencillaatsicqkkan 269

RESULT 6
 ID AAY24151
 AC AAY24151; standard; Protein; 273 AA.

XX
 XX 10-SEP-1999 (first entry)
 DT
 XX Human LDL receptor.
 DE
 XX Human; LDL; denatured; oxidized; arteriosclerosis; hyperlipidaemia;
 KM low density lipoprotein; receptor; detection; immunoglobulin;
 KM fusion protein.
 XX
 OS Homo sapiens.
 XX
 PN WO9332520-A1.
 XX
 PD 01-JUL-1999.
 XX
 PF 18-DEC-1998; 98WO-JP05744.
 XX
 PR 16-DEC-1998; 98JP-0358170.
 PR 19-DEC-1997; 97JP-0364981.

PR 09-DEC-1998; 98JP-0349648.
 XX
 PA (NISB) JAPAN TOBACCO INC.
 XX
 XX Kakutani M, Masaki T, Sawamura T;
 PI
 XX MPI: 1999-418906/35.
 DR N-PSDB; AAX88527.
 XX
 XX Fusion peptide for assay of oxidized LDL and for therapeutic use
 PT
 PS Claim 9; Page 71-73; 105pp; Japanese.
 XX

CC The present invention describes a fusion peptide which consists of the
 CC extracellular domain of a mammalian oxidized LDL (low density
 CC lipoprotein) receptor, fused to a partial heavy chain of a mammalian
 CC immunoglobulin containing all or part of the constant region. Oxidized
 CC LDL is a denatured form of LDL occurring in patients having
 CC arteriosclerosis or hyperlipidaemia, and the fusion peptide can be
 CC used for the assay of oxidized LDL in biological samples from such
 CC patients, for the diagnosis of the disorders. It can also be used
 CC therapeutically for the prevention and treatment of arteriosclerosis and
 CC hyperlipidaemia. The present sequence represents the human LDL receptor.
 XX
 CC Sequence 273 AA:

Query Match 48.1%; Score 635; DB 20; Length 273;
 Best Local Similarity 48.5%; Pred. No. 2.6e-45;
 Matches 133; Conservative 36; Mismatches 69; Indels 36; Gaps 6;

QY 1 MTFDD-KMKPANDPPDKSGKKPKESORELK-----GKIDT-- 37
 DB 1 mtfddkikgtvkdpqeksnqkka-----gldflyspwlaaatlgvclgvlvltlmv 55
 QY 38 -----TRKLDEKSKQEDELQMIQNLQ---EALQRAANSSEESORELKIDITLTKLNE 90
 DB 56 lmqqlsqvsdlltqeganltqkkllegqtsarqaeasqesenelekmetarkline 115
 QY 91 KSKQEDELQKQNLQALQRAANFSGPCQDMLMKENCYLF-HGPFGEKRNQTCQSL 149
 DB 116 ksqegmelhqnlnlqetlkrvancsapcpqdwlmhngencyltsqsfmweksqekcls1 175
 QY 150 GGQLQINGADDLFTILQAISSHSTSPFWIGLHRRKKGQPLWENGTPPLNFQFRTGVS 209
 DB 176 dakllkinstadldlfgqatsysfpmglstrnpsypwlvwedgspjlmphlfrvgavs 235
 QY 210 QLYSSNCAYLDGAVFAENCILIASFCOKTN 243
 DB 236 qlypsgtcaylgrgavyaencillaatsicqkkan 269

RESULT 7
 ID AAR9586
 AC AAR9586; standard; Protein; 270 AA.

XX
 XX 29-OCT-1996 (first entry)
 DT
 XX Low density lipoprotein receptor.
 DE
 XX LDL; low density lipoprotein; receptor; bovine; assay; detection;
 KM recombinant production; haemangioendothelial cell.
 KM
 OS Bos taurus.
 XX
 PN WO9617058-A1.
 XX
 PD 06-JUN-1996.
 XX
 PR 30-NOV-1995; 95WO-JP02444.

PR 31-JUL-1995; 95JP-0214206.
PR 30-NOV-1994; 94JP-0321705.
XX
PA (NICH) NIPPON CHEMIPHAR CO.
XX
PI Masaki T, Sawamura T;
XX
XX WPI: 1996-277778/28.
DR N-PSDB; AAT32576.
XX
PT DNA encoding denatured low-density lipoprotein receptor of mammalian
PT haemangioma endothelial cells - useful for generating antibodies for
PT use in detection of LDL in biological samples
XX
XX
PS Claim 1; Page 22-26; 44pp; Japanese.
CC The present sequence is that of a bovine denatured low density
CC lipoprotein (LDL) receptor encoded by DNA isolated from
CC haemangioma endothelial cells. The DNA is useful for the production of
CC the receptor protein in transformed hosts. Antibodies to the protein
CC are useful in detection and assays of LDL in biological samples.
XX
XX Sequence 270 AA;

Query Match 45.2%; Score 596; DB 17; Length 270;
Best Local Similarity 44.6%; Pred. No. 4.7e-42;
Matches 125; Conservative 39; Mismatches 70; Indels 46; Gaps 6;

QY 1 MTFDDKMKRANDEPDOKSGKKPK-----EESQR 29
Db 1 mtfvddp-kymkdqldqkpnktakgfvswrwyapaavlgyclgllytvvlllllqlsq- 58
QY 30 ELKGRIDITRKLDKSKKEQELL--QMIONLOEALORANSSSESSORELKGIDITLTK 87
Db 59 -----vsdlkkqgnlthgedilegqll-----agrrseksaqesqkelkemieltiahk 108
QY 88 INEKSKEQELLQKNONLOEALORANFSGPCPODMLWHKENCYLF-HGPFGEKKNROTG 146
Db 109 ldekskkmelhrgnlhqlnqevlkeaanysgpcpqdwlwheencyfssgfweksqenc 168
QY 147 OSLSGQLQINGADDLFTFLQAISSHTTSPFWIGLHRRKRGQWLMENGTPLNFOFFKTRG 206
Db 169 lslahllklnstdeletlqgmiahnsfpmgmjmsmrkpnyswlwedgtplphlfrlqg 228
QY 207 VSLQLYSSNCAYLQDGAFFAENCILIAFSICOKKTNHLQ 246
b 229 avsrmypsgtcaylqrgtvaencillatatsicqkkanllr 268

RESULT 8
AAY24152
ID AAY24152 standard; Protein: 270 AA.
XX
AC AAY24152;
XX
DT 10-SEP-1999 (first entry)
XX
DE Bovine LDL receptor.
XX
XX LDL; denatured; oxidised; arteriosclerosis; hyperlipidaemia;
KW low density lipoprotein; receptor; detection; immunoglobulin;
KM fusion protein.
XX
OS Bos sp.
XX
XX WO9932520-A1.
XX
XX 01-JUL-1999.
XX
XX 18-DEC-1998; 98MO-JP05744.
XX
XX 16-DEC-1998; 98JP-0358170.
XX
XX

PR 19-DEC-1997; 97JP-0364981.
PR 09-DEC-1998; 98JP-0349648.
XX
XX
PA (NITSB) JAPAN TOBACCO INC.
XX
XX
PI Kakutani M, Masaki T, Sawamura T;
XX
XX WPI: 1999-418906/35.
DR N-PSDB; AAB85828.
XX
XX
XX Fusion peptide for assay of oxidized LDL and for therapeutic use
PT
PS Claim 11; Page 73-75; 105pp; Japanese.

CC The present invention describes a fusion peptide which consists of the
CC extracellular domain of a mammalian oxidized LDL (low density
CC lipoprotein) receptor, fused to a partial heavy chain of a mammalian
CC immunoglobulin containing all or part of the constant region. Oxidized
CC LDL is a denatured form of LDL occurring in patients having
CC arteriosclerosis or hyperlipidaemia, and the fusion peptide can be
CC used for the assay of oxidized LDL in biological samples from such
CC patients, for the diagnosis of the disorders. It can also be used
CC therapeutically for the prevention and treatment of arteriosclerosis and
CC hyperlipidaemia. The present sequence represents the bovine LDL receptor.
XX
XX Sequence 270 AA;

Query Match 45.2%; Score 596; DB 20; Length 270;
Best Local Similarity 44.6%; Pred. No. 4.7e-42;
Matches 125; Conservative 39; Mismatches 70; Indels 46; Gaps 6;

QY 1 MTFDDKMKRANDEPDOKSGKKPK-----EESQR 29
Db 1 mtfvddp-kymkdqldqkpnktakgfvswrwyapaavlgyclgllytvvlllllqlsq- 58
QY 30 ELKGRIDITRKLDKSKKEQELL--QMIONLOEALORANSSSESSORELKGIDITLTK 87
Db 59 -----vsdlkkqgnlthgedilegqll-----agrrseksaqesqkelkemieltiahk 108
QY 88 INEKSKEQELLQKNONLOEALORANFSGPCPODMLWHKENCYLF-HGPFGEKKNROTG 146
Db 109 ldekskkmelhrgnlhqlnqevlkeaanysgpcpqdwlwheencyfssgfweksqenc 168
QY 147 OSLSGQLQINGADDLFTFLQAISSHTTSPFWIGLHRRKRGQWLMENGTPLNFOFFKTRG 206
Db 169 lslahllklnstdeletlqgmiahnsfpmgmjmsmrkpnyswlwedgtplphlfrlqg 228
QY 207 VSLQLYSSNCAYLQDGAFFAENCILIAFSICOKKTNHLQ 246
Db 229 avsrmypsgtcaylqrgtvaencillatatsicqkkanllr 268

RESULT 9
AAB85870
ID AAB85870 standard; Protein: 270 AA.
XX
AC AAB85870;
XX
DT 30-NOV-2001 (first entry)
XX
DE Bovine LOX-1 polypeptide.
XX
XX LOX-1; LDL; monoclonal antibody; low density lipoprotein; human;
KW arteriosclerosis; cardiovascular; kidney disease; inflammatory disorder;
KM leukocyte; bovine.
XX
OS Bos taurus.
XX
XX WO200164862-A1.
XX
XX 07-SEP-2001.
XX
XX

PF 02-MAR-2001; 2001WO-JP01636.
XX
XX 02-MAR-2000; 2000JP-0057745.
PR 31-OCT-2000; 2000JP-0333116.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Kobayashi Y, Tsuji H, Kamada M, Sawamura T;
PI
XX WPI; 2001-565503/63.
XX N-PSDB; AAA47106.
DR
XX
XX Human monoclonal antibodies recognizing oxidized low density
PT lipoprotein receptor for treatment of atherosclerosis and
PT cardiovascular and kidney diseases
XX
XX
XX Disclosure: Page 94-98; 131pp; Japanese.
XX
XX The invention provides human monoclonal antibodies and their fragments
CC binding to human oxidized low density lipoprotein (LDL) receptor (LOX-1),
CC and inhibiting intracellular binding of the receptor to oxidized LDL.
CC Drug compositions containing the MAb are useful in the treatment and
CC prevention of atherosclerosis, cardiovascular and kidney diseases,
CC inflammatory disorders and infiltration of leukocytes. The present
CC sequence represents a bovine LOX-1 polypeptide.
XX
SQ Sequence 270 AA:

Query Match 45.2%; Score 596; DB 22; Length 270;
Best Local Similarity 44.6%; Pred. No. 4.7e-42;
Matches 125; Conservative 39; Mismatches 70; Indels 46; Gaps 6;
QY 1 MTFDDKKRPANDEPDOKSCGKKPK-----EESQR 29
|| || | : || | || |
Db 1 mtyddp-kgmkddqldqpgnkktakgfyvswrwyapaavlglciglvtvlllllql 58
|| || | : || | || |
QY 30 ELKGKIDITRKLDKESKEQELL--OMIONLOALORANSSSESGRELKGTDTLTK 87
|| || | : || | || |
Db 59 -----vsdlkkqganltbgedlllegqll-----agtrseksaqesqkelkemtlatkh 108
|| || | : || | || |
QY 88 LNEKSKQEELLKQNONLOALORANFSGPCPODWLWHEKNCYLF-HGPFGEKKNRQTC 146
|| || | : || | || |
Db 109 ldekskklmeihrgnlnlgevlkeaanysgpcpqlwheencyfssgsfnwksq 168
|| || | : || | || |
QY 147 QSLGQLQINGADLFTLQAIHTTSPWIGLHRRKPGQPLWENGTPUNFOFFKTRG 206
|| || | : || | || |
Db 169 lslidahlklnstdelefqgmahsfpfwmjlsmkpnywledtrpltpflfr 228
|| || | : || | || |
QY 207 VSIQLYSSNCAYLQDGAFAENCILIAFSICOKKTNHLO 246
|| || | : || | || |
Db 229 avarmypsgtcaylqgrvtfaencillatfscqkkanllr 268
|| || | : || | || |

RESULT 10
AA99587
ID AAR99587 standard; Protein; 273 AA.
XX
XX AAR99587;
AC
XX
XX 29-OCT-1996 (first entry)
DT
XX
XX Low density lipoprotein receptor.
DE
XX
XX LDL; low density lipoprotein; receptor; bovine; assay; detection;
KW recombinant production; haemangioendothelial cell.
XX
XX Bos taurus.
OS
XX
XX WO9617058-A1.
PN
XX
XX 06-JUN-1996.
PD
XX

PF 30-NOV-1995; 95WO-JP02444.
XX
XX 31-JUL-1995; 95JP-0214206.
PR 30-NOV-1994; 94JP-0321705.
XX
XX (NICM) NIPPON CHEMIPHAR CO.
XX
XX Masaki T, Sawamura T;
PI
XX WPI; 1996-277778/28.
XX N-PSDB; AAT32577.
DR
XX
XX DNA encoding denatured low-density lipoprotein receptor of mammalian
PT haemangioendothelial cells - useful for generating antibodies for
PT use in detection of LDL in biological samples
XX
XX
XX Claim 1; Page 27-30; 44pp; Japanese.
XX
XX The present sequence is that of a bovine denatured low density
CC lipoprotein (LDL) receptor encoded by DNA isolated from
CC haemangioendothelial cells. The DNA is useful for the production of
CC the receptor protein in transformed hosts. Antibodies to the protein
CC are useful in detection and assays of LDL in biological samples.
XX
SQ Sequence 273 AA:

Query Match 45.1%; Score 594.5; DB 17; Length 273;
Best Local Similarity 44.2%; Pred. No. 6.4e-42;
Matches 125; Conservative 39; Mismatches 70; Indels 49; Gaps 6;
QY 1 MTFDDKKRPANDEPDOKSCGKKPK-----EE 26
|| || | : || | || |
Db 1 mtyddp-kgmkddqldqpgnkktakgfyvswrwyapaavlglciglvtvlllllql 59
|| || | : || | || |
QY 27 SQRELKIDITRKLDKESKEQELL--OMIONLOALORANSSSESGRELKGTDTLTK 84
|| || | : || | || |
Db 60 sq-----vsdlkkqganltbgedlllegqll-----agtrseksaqesqkelkemtlatkh 108
|| || | : || | || |
QY 85 TLKLEKSKQEELLKQNONLOALORANFSGPCPODWLWHEKNCYLF-HGPFGEKKNR 143
|| || | : || | || |
Db 109 ahkldeskkklmeihrgnlnlgevlkeaanysgpcpqlwheencyfssgsfnwksq 168
|| || | : || | || |
QY 144 QTCOSLQQLQINGADLFTLQAIHTTSPWIGLHRRKPGQPLWENGTPUNFOFFK 203
|| || | : || | || |
Db 169 encsltahllklnstdelefqgmahsfpfwmjlsmkpnywledtrpltpflfr 228
|| || | : || | || |
QY 204 TRGSILQYSSNCAYLQDGAFAENCILIAFSICOKKTNHLO 246
|| || | : || | || |
Db 229 lqgavstrmypsctcaylqgrvtfaencillatfscqkkanllr 271
|| || | : || | || |

RESULT 11
AA924153
ID AAY24153 standard; Protein; 445 AA.
XX
XX AAY24153;
AC
XX
XX 10-SEP-1999 (first entry)
DT
XX
XX Bovine LOX-1 extracellular region/human IgG1 Fc region chimeric protein.
DE
XX
XX LDL; denatured; oxidised; arteriosclerosis; hyperlipidaemia;
KW low density lipoprotein; receptor; detection; immunoglobulin;
KW fusion protein; chimeric protein.
XX
XX Chimeric - Bos sp.
OS
XX
XX Chimeric - Homo sapiens.
PN
XX
XX WO9332520-A1.
PD
XX
XX 01-JUL-1999.

XX	23-SEP-1999.
XX	
PE	16-MAR-1999; 99MO-US03740.
XX	
PR	17-MAR-1998; 980S-0040111.
XX	
PA	(SCHE) SCHERING CORP.
XX	
PI	Chalus L, Quan AB, Bates EEM, Gorman DM, Saeland S, Lebeque SJE,
PI	Phillips JH;
XX	
DR	WPI; 1999-562114/47.
DR	N-PsDB; AA0207533.
XX	
PT	Binding compound specific for primate or rodent Schering dendritic cell
PT	membrane proteins _
PS	
XX	Claim 2; Page 84-85; 89pp; English.
XX	
CC	The invention relates to a binding compound comprising an antibody
CC	binding site which specifically binds to: (a) a primate or rodent
CC	Schering dendritic cell membrane protein 3 (SDCMP3) protein; or (b) a
CC	primate SDCMP4 protein. The binding compound can be used to modulate
CC	dendritic cell physiology or function. The sequences may also be used as
CC	probes in forensic techniques, such as genetic fingerprinting. They can
CC	also be used to distinguish tissue and cell types in situ or in vitro.
CC	The sequences may also be useful in cancer immunotherapy and in the
CC	treatment of conditions associated with abnormal physiology or
CC	degenerative, including abnormal proliferation, e.g. cancerous conditions
CC	SDCMP4 polypeptide (lectin 47).
XX	
XX	Sequence 247 AA;

[illegible]

RESULT	13
AAW73889	
ID	AAW73889 standard; Protein: 247 AA.
XX	
AC	AAW73889;
XX	
DT	31-MAR-1999 -(first entry)
XX	
DE	Human DC3' protein sequence.
XX	
KW	Dendritic cell-derived membrane protein; human; DC3'.
XX	
OS	Homo sapiens.
XX	
PN	JF11001497-A.
XX	
PD	06-JAN-1999.
XX	
PF	13-JUN-1997; 97JP-0156376.
XX	
PR	13-JUN-1997; 97JP-0156376.

xx	PA	(TAKE) TAKEDA CHEM IND LTD.
xx	DR	WPI: 1999-125479/11.
xx	DR	N-PSDB: NAX01260.
xx	PT	New membrane protein and its DNA - useful as reagents for screening
xx	PT	ligand, agonist or antagonist
xx	PS	Claim 1; Page 37-38; 44pp; Japanese.
xx	CC	This sequence is the human dendritic cell-derived membrane protein
xx	CC	DC3' of the invention. The protein, its fragments and salts are useful a
xx	CC	reagents for screening a ligand, an agonist or an antagonist DC3.
xx	SO	Sequence 247 AA;
xx	Qy	Query Match 19.6%; Score 258; DB 20; Length 247;
xx	Db	Best Local Similarity 31.2%; Pred. No. 9.5e-14;
xx	Matches	50; Conservative 41; Mismatches 65; Indels 4; Gaps
xx	Qy	86 LKLNKSKEDQ--ELLQKKNQNLQDALQRAANFSGPCQDMLMKENCYLPHGPF-GWEKN 142
xx	Db	85 Lsrkknmsqptqslsdsvtpkavktlcvlsspcppmwllyekscylfmslnsdgs 144
xx	Qy	143 RQTCOSLQGLQINGADDLFEIL-QAISHTSPFVIGLHRRKPGQPMWENCTPLNFOF 201
xx	Db	145 krqcgqqlgnslkkdsanelsglvkysqpdnsfwglarptqetpwlwedgstfssnl 204
xx	Qy	202 FKTRGVSLQLYSSSNCAVLQDGAFAENCILIAFSTQKR 241
xx	Db	205 fqlrtalcqenpspcwlvhsvlyldqlcsvpsyslcek 244
xx	RESULT 14	
xx	AAM52837	
xx	ID	AAM52837 standard; Protein; 201 AA.
xx	AC	AAM52837;
xx	DT	24-JUN-1998 (first entry)
xx	DE	Human C-type lectin MCTL.
xx	KM	C-type lectin; MCTL; type II membrane protein; antibody;
xx	KW	diagnosis; Antisense; allograft; macrophage.
xx	OS	Homo sapiens.
xx	PK	W09802456-A2.
xx	PD	22-JAN-1998.
xx	PF	15-JUL-1997; 97MO-US12342.
xx	PR	30-JUL-1996; 96US-0688342.
xx	PR	15-JUL-1996; 96US-0683657.
xx	PA	(INCY-) INCYTE PHARM INC.
xx	PI	Au-young J, Cocks BG, Goli SK, Hllman JL;
xx	DR	WPI: 1998-110526/10.
xx	DR	N-PSDB: AAV21156.
xx	PT	Human C-type lectin - useful in, e.g. treating graft rejection,
xx	PT	auto-immune disease and cancer
xx	PS	Claim 1; Fig 1; 53pp; English.
xx	CC	The human C-type lectin MCTL protein shows homology to the C-type lectin
xx	CC	superfamily of type II membrane proteins. Purified MCTL and its

[illegible]

CC treatment of conditions associated with abnormal physiology or
 CC development, including abnormal proliferation, e.g. cancerous conditions,
 CC or degenerative conditions. The present sequence represents the human
 CC SDCMP4 short form polypeptide (alternative splice form).

XX Sequence 201 AA;

Query Match 19.0%; Score 251; DB 20; Length 201;
 Best Local Similarity 35.2%; Pred. No. 2.8e-13;
 Matches 45; Conservative 32; Mismatches 49; Indels 2; Gaps 2;

OY 116 SGPCEPDWIMHKNKCYLFHGPFGWEKNRQTCOSLGQDLQINGADLTFIL-QAISHTT 173
 | | | | : : : : | | | | : : : | | | | : : : | | | | : : : |
 DB 71 sspcpnwliyekscylfamslnswdgskrqcmqlgsnllkldsanelgfvkqvssqpd 130
 OY 174 SPFWIGLHRRKKRGGQPLWENGTPPLNFQEPFKTRGVSLQLYSSNCAYLQDGA VFAENCIL I 233
 : : : : | | | | : : : : | | | | : : : | | | | : : : | | | | : : : |
 DB 131 nsfwiglsrptqevpwlwedgstfssnlfqirtatqenpsncwlvhsvlydqlcsvp 190
 OY 234 AFSICOKK 241
 : : : : | | | | : : : : | | | | : : : | | | | : : : | | | | : : : |
 DB 191 sysicekk 198

Search completed: August 19, 2002, 22:57:18
 Job time: 3580 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 19, 2002, 22:01:29 ; Search time 25.02 seconds
(without alignments)
-241.132 Million cell updates/sec

Title: US-09-898-554-14

Perfect score: 1319

Sequence: 1 MFEDDKMKPANDPEDQKSCG.....ENCILIAFSICQKTNHLQI 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued_Patents_AA.*
2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	637	48.3	273	2	US-09-055-095-3
2	637	48.3	273	2	US-08-809-494A-6
3	637	48.3	273	4	US-09-352-302-6
4	596	45.2	270	2	US-09-055-095-4
5	596	45.2	270	2	US-08-809-494A-2
6	596	45.2	270	4	US-09-352-302-2
7	594.5	45.1	273	2	US-08-809-494A-4
8	594.5	45.1	273	4	US-09-352-302-4
9	251	19.0	201	2	US-08-688-342-1
10	251	19.0	201	2	US-09-113-788-1
11	231.5	17.6	180	3	US-08-772-440-31
12	231	17.5	176	3	US-08-772-440-8
13	231	17.5	244	3	US-08-772-440-2
14	221	16.8	284	2	US-09-055-095-1
15	214	16.2	199	3	US-08-772-440-13
16	207	15.7	126	3	US-08-772-440-10
17	189.5	14.4	122	3	US-08-722-126A-9
18	189.5	14.4	122	5	PCT-US95-04258-9
19	186	14.1	272	5	US-08-690-095-1
20	186	14.1	272	3	US-09-113-789-1
21	186	14.1	287	1	US-08-365-103B-4
22	186	14.1	300	1	US-08-365-103B-6
23	186	14.1	327	1	US-08-365-103B-2
24	179	13.6	229	4	US-09-247-155-97
25	166	12.6	179	1	US-08-690-095-9
26	166	12.6	179	1	US-08-650-578-2
27	166	12.6	179	2	US-08-688-342-3

28	166	12.6	179	2	US-09-113-788-3	Sequence 3, Appli
29	166	12.6	179	3	US-09-113-789-9	Sequence 9, Appli
30	165.5	12.5	287	4	US-09-111-470-6	Sequence 6, Appli
31	165.5	12.5	320	1	US-08-365-103B-10	Sequence 10, Appli
32	165.5	12.5	321	1	US-08-365-103B-8	Sequence 8, Appli
33	162.5	12.3	231	1	US-08-690-095-6	Sequence 6, Appli
34	162.5	12.3	231	3	US-09-113-789-6	Sequence 6, Appli
35	162.5	12.3	231	4	US-08-543-246B-6	Sequence 6, Appli
36	162.5	12.3	231	4	US-08-543-246B-23	Sequence 23, Appli
37	158.5	12.0	134	4	US-08-543-246B-20	Sequence 20, Appli
38	158.5	12.0	216	4	US-08-543-246B-9	Sequence 9, Appli
39	158.5	12.0	216	4	PCT-US93-10418-24	Sequence 24, Appli
40	154.5	11.7	199	5	PCT-US93-10418-2	Sequence 2, Appli
41	154	11.7	115	3	US-08-722-126A-8	Sequence 8, Appli
42	154	11.7	115	5	PCT-US95-04258-8	Sequence 8, Appli
43	150	11.4	1479	3	US-08-840-062-4	Sequence 4, Appli
44	149.5	11.3	233	1	US-08-690-095-8	Sequence 8, Appli
45	149.5	11.3	233	3	US-09-113-789-8	Sequence 8, Appli

ALIGNMENTS

```
RESULT 1
US-09-055-095-3
; Sequence 3, Application US/09055095
; Patent No. 5945308
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Patterson, Chandra
; APPLICANT: Corley, Neil C.
; APPLICANT: Sathier, Susan
; TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/055,095
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0500 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-845-4166
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1902984
US-09-055-095-3
Query Match 48.3%; Score 637; DB 2; Length 273;
```

Best Local Similarity 48.9%; Pred. No. 1.5e-49;
Matches 134; Conservative 35; Mismatches 69; Indels 36; Gaps 6

QY	1	MTDQ-KKKPANDPDDQSCCKKREESORBLK	-----	-GKIDT- -	38
		: : : : : :		:	
Dp	1	MTPDLLQIQTAKDQDDEKSNKKAK	-----	-GLOFLYSPWMLAANTIGVLCGLVITIM	55
QY	39	-----TKRLDEKSKQEQLLMIQNLQ---	-BALORPANSSESORBLKGDITDITLTKLNE		90
		: : : :	: : : :	:	
Dp	56	LGMOLSOYSDLLTQEQALWTHQKKLEQIISAROOAEASOSENELEKMETETARKLNE			115
QY	91	KSKEEELLQKNNLOEALORAPNSGCPDMDLHKENCYLF-	-HGPEGKEKNPOTOSL		145
		: : : : :	: : : :	:	
Dp	116	KSKEGEMELHONLNLQETLTKRYVANCASACPDPDWTIHGENCITLFFSGSFNMEKSOEKCLSL			175
QY	150	GGQLLQINGADDLFTILQAISSHSTSPFWIGLHKRRKPGQPMWLMNGTPINFLQFETKRGVSL			205
		: : : : :	: : : :	:	
Dp	176	DAKLKINSTADDLFTIOQAISSYSPFPMGMSRRNPSPYMLMEDGSPMLPHLFRGAVS			235
QY	210	QLYSSNCAYLQDGAVFAPENCLILAFSTCOCKTN			243
		: : : : :	: : : :	:	
Dp	236	QTYPSGTCAVYIQRGAVVAENCLILAFSTCOCKKAN			269

RESULT 2
TIC-08-000

```

Sequence 6, Application US/0809494A
Patent No. 5962260

GENERAL INFORMATION:
APPLICANT: Sawamura, Tatsuya
APPLICANT: Masaki, Tomoo
TITLE OF INVENTION: Modified Low-Density Lipoprotein
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAlley Fisher Nissen Goldberg & Kiel
STREET: 261 Madison Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,494A
FILING DATE: 24-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-321705
FILING DATE: 30-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-214206
FILING DATE: 31-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Goldberg, Jules E
REGISTRATION NUMBER: 24408
REPRESENTATION/DOCKET NUMBER: JG-YY-4363PCL
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 986-4090
TELEFAX: 212 818-9479
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-809-494A-6

```

Query Match 48.3%; Score 637; DB 2; Length 273;

Best Local Similarity 48.9%; Pred. No. 1.5e-49;
Matches 134; Conservative 35; Mismatches 69; Indels 36; Gaps 6

```

QY 1 MTFPD-KMKRPANDPDCKCKKREESORELK-----CKIDT-- 38
      ||||| : : :||| ||| : :||| : :|||
Db 1 MTFPDLLKIQYKDDPDEKSNCKKAK-----GLQZLYSPMCMCLAAATLYGVLCLGLVATIMV 55
      ||||| : : :||| ||| : :||| : :|||
QY 39 -----TRKDEKSKOEELLOMIQNO--EALQRAANSSEESORELKXIDTLYTKLNE 90
      : : :||| : :||| : :||| : :||| : :|||
Db 56 LGMOLSOVSDLLTFOEALNLTTHOKKLLGQISARQAEASQESFENELKEMLETTLARKNE 115
      ||||| : : :||| ||| : :||| : :||| : :|||
QY 91 KSKROEELLOKNLOLOEAANFSPCPDDMYLMEHCNYLF-HGPFGEKXNRQCSOL 149
      ||||| : :||| : :||| : :||| : :||| : :||| : :|||
Db 116 KSKQDMLEHHOBNLMQLETLKRVANCSAPCPDDMYLMEHCNYLTVSSGFSNMEKSOEKLSL 175
      ||||| : :||| : :||| : :||| : :||| : :||| : :|||
QY 150 GGOULLINGADDLFFILLOAISHTTPSPWIGLHRKKPCQPMWLMNGTFLNQQFETKTRVSL 209
      : :||| : :||| : :||| : :||| : :||| : :||| : :|||
Db 176 DAKLLKINSTADLDFIQOATISSYSPFMWGLSRNRPSPYMLMEDGSPMLPHLFRVRKAVS 235
      ||||| : :||| : :||| : :||| : :||| : :||| : :|||
QY 210 QLYSSSCATLYQDCAVPAENCILIAESTICOKTIN 243
      ||||| : :||| : :||| : :||| : :||| : :||| : :|||
Db 236 QTYPSGTCAVLYQRGAVYAENCILIAESTICOKKAN 269
      ||||| : :||| : :||| : :||| : :||| : :||| : :|||

```

RESULT 3

Sequence 6, APPLICATION US/09352302
Patent No. 6197937
GENERAL INFORMATION:
APPLICANT: Sawamura, Tatsuya
APPLICANT: Masaki, Tomoo
TITLE OF INVENTION: Modified Low-Density Lipoprotein
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAlail Fisher Nissen Goldberg & Kiel
STREET: 261 Madison Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/352,302
FILING DATE: 12-JUL-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-321705
FILING DATE: 30-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-214206
FILING DATE: 31-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Goldberg, Jules E
REGISTRATION NUMBER: 24408
REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 986-4090
TELEFAX: 212 818-9479
INFORMATION FOR SEQ ID NO.: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

Query Match 48.38; Score 637; DB 4; Length 273;

Best Local Similarity 48.9%, Pred. No. 1.5e-49;
Matches 134; Conservative 35; Mismatches 69; Indels 36; Gaps 6;

```

QY 1 MFDD-KMKPANDPPDCKSGKKPKESQRELK-----GKIDTI--38
   ||||| : : : ||||| : : : ||||| : : : ||||| : : : ||
Db 1 MFDDKKTQTVADQDPDKSNGKKAK-----GLQFLYSPMWCILAAATLGLVCLGVVTV 55
   ||||| : : : ||||| : : : ||||| : : : ||||| : : : ||
QY 39 -----TRKLEDSKEQELLQMIQNLQ-----EALQRAANSSESORELKGKIDTLTLK 90
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 56 LGMQISQYSDLLTQDQANTHQKKLEQISARQQAESAQSESNELKEMITLAKKLN 115
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 91 KSEQELLQKQNLQEAQRAANFSGPCQDMLMKENCYLF-HGPFGEKNRQTC 149
   ||||| : : : ||||| : : : ||||| : : : ||||| : : : ||
Db 116 KSEQEMELHQNLQETLKRVAANCSAPCPQDMLMKENCYLFSSGSGFMWKSQEKCL 175
   ||||| : : : ||||| : : : ||||| : : : ||||| : : : ||
QY 150 GGLQINGADLFTFLQISHTSPFWGLHRKKPCQDMLMKENCYLFNPFQFKTGS 209
   ||||| : : : ||||| : : : ||||| : : : ||||| : : : ||
Db 176 DAKLKINSTADLFTQQAISTSPFWGLSRNPSYFWLWEDGSPMLPFLRVGAVS 235
   ||||| : : : ||||| : : : ||||| : : : ||||| : : : ||
QY 210 QLYSSNCAYLQDGAFAENCILIAFSICOKKTN 243
   ||||| : : : ||||| : : : ||||| : : : ||||| : : : ||
Db 236 QYPSGTCAVIGRGAVYAENCILIAFSICOKKAN 269
   ||||| : : : ||||| : : : ||||| : : : ||||| : : : ||

```

RESULT 4

```

; US-09-055-095-4
; Sequence 4, Application US/09055095
; Patent No. 5945308
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Patterson, Chandra
; APPLICANT: Corley, Neil C.
; APPLICANT: Sather, Susan
; TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/055.095
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0500 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-845-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1902982
; US-09-055-095-4

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Query Match 45.2%; Score 596; DB 2; Length 270;
Best Local Similarity 44.6%; Pred. No. 7.1e-46;
Matches 125; Conservative 39; Mismatches 70; Indels 46; Gaps 6;

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QY 1 MFDDKMKPANDPPDCKSGKKPK-----ESQR 29
   ||||| : : : ||||| : : : ||||| : : : ||||| : : : ||
Db 1 MVDVDP-KMKQDQDLPKNGKTAQGVSSRWYPAATVTLGLVCLGVVTVILLILOLSO- 58
   ||||| : : : ||||| : : : ||||| : : : ||||| : : : ||
QY 30 ELKGRKIDTLRKLEDSKEQELL--QMIONQEAQRAANSSESORELKGKIDTLTLK 87
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 -----VSLDKKQQAANTHOEDILEGQIL-----AQRSEKSAQESQELKEMITLAK 108
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 88 LNEKSEQELLQKQNLQEAQRAANFSGPCQDMLMKENCYLF-HGPFGEKNRQTC 146
   ||||| : : : ||||| : : : ||||| : : : ||||| : : : ||
Db 109 LDEKSKLMEHLHQNLQEAQRAANFSGPCQDMLMKENCYLFSSGSGFMWKSQEK 168
   ||||| : : : ||||| : : : ||||| : : : ||||| : : : ||
QY 147 OSQGLQINGADLFTFLQISHTSPFWGLHRKKPCQDMLMKENCYLFNPFQFKTGS 206
   ||||| : : : ||||| : : : ||||| : : : ||||| : : : ||
Db 169 LSLDAHLKINSTDELEFTQQAISTSPFWGLSRNPSYFWLWEDGSPMLPFLRV 228
   ||||| : : : ||||| : : : ||||| : : : ||||| : : : ||
QY 207 VSLQYSSNCAYLQDGAFAENCILIAFSICOKKTN 246
   ||||| : : : ||||| : : : ||||| : : : ||||| : : : ||
Db 229 AVSRMTPSGTCAYIGRGAVYAENCILIAFSICOKKAN 268
   ||||| : : : ||||| : : : ||||| : : : ||||| : : : ||

```

RESULT 5

```

; US-08-809-494A-2
; Sequence 2, Application US/08809494A
; Patent No. 5962260
; GENERAL INFORMATION:
; APPLICANT: Sawamura, Tatsuya
; APPLICANT: Masaki, Tomoo
; TITLE OF INVENTION: Modified Low-Density Lipoprotein
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAlay Fisher Nissen Goldberg & Kiel
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,494A
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-321705
; FILING DATE: 30-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-214206
; FILING DATE: 31-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldberg, Jules E.
; REGISTRATION NUMBER: 24408
; REFERENCE/DOCKET NUMBER: JG-YY-4363PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 986-4090
; TELEFAX: 212 818-9479
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-494A-2

```

Query Match 45.2%; Score 596; DB 2; Length 270;
Best Local Similarity 44.6%; Pred. No. 7.1e-46;
Matches 125; Conservative 39; Mismatches 70; Indels 46; Gaps 6;

QY 1 MTFDDKMPANDEPDOKSCGKKPK-----EESQR 29
DB 1 MTFDDP-KGMRDQDQKNGKTAKGVSSWRWYPAAVTLGVLGLLTVILLILOLSQ- 58
QY 30 ELKGIKIDITTRKLEKSEKEOEEL--OMIONLOEALORANSESEORRELKGIKIDITLTK 87
DB 59 -----VSLIKKQOANTHODILEGQIL-----AQRSEKSAQESQKELKEMETLAKH 108
QY 88 LNEKSKOEELLKQNLQLEALORANFSGPCPODWIMHKENCYLF-HGPGMEKNQTC 146
DB 109 LDEKSKLMEHLRONLNLQEVLEKAAVSGPCPODWIMHEENCYQFSSGSFMEKESQENC 168
QY 147 QSLGGOLQINGADDLFTIILQAIHTTSPFVIGLHRRKPGCPWIMENGTPLNPFKTRG 206
DB 169 LSLDAHLKLNSTDELEFIQMIHASSPFWGLSMRKNYSWLMEGDTPLPHLFRIOG 228
QY 207 VSLQVSSNCAYLQDGAFAENCILIAFSICOKKTNHLQ 246
DB 229 AVSRMPSGTCAYIQRGTVFAENCILIAFSICOKKANILR 268

RESULT 6
US-09-352-302-2
; Sequence 2, Application US/09352302
; Patent No. 6197937
; GENERAL INFORMATION:
; APPLICANT: Sawamura, Tatsuya
; TITLE OF INVENTION: Modified Low-Density Lipoprotein
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAlay Fisher Nissen Goldberg & Kiel
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/352,302
; FILING DATE: 12-JUL-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-321705
; FILING DATE: 30-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-214206
; FILING DATE: 31-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldberg, Jules E
; REGISTRATION NUMBER: 24408
; REFERENCE/DOCKET NUMBER: JG-Y-4363PCT/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 986-4090
; TELEFAX: 212 818-9479
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-352-302-2

Query Match 45.2%; Score 596; DB 4; Length 270;
Best Local Similarity 44.6%; Pred. No. 7.1e-46;
Matches 125; Conservative 39; Mismatches 70; Indels 46; Gaps 6;

QY 1 MTFDDKMPANDEPDOKSCGKKPK-----EESQR 29
DB 1 MTFDDP-KGMRDQDQKNGKTAKGVSSWRWYPAAVTLGVLGLLTVILLILOLSQ- 58
QY 30 ELKGIKIDITTRKLEKSEKEOEEL--OMIONLOEALORANSESEORRELKGIKIDITLTK 87
DB 59 -----VSLIKKQOANTHODILEGQIL-----AQRSEKSAQESQKELKEMETLAKH 108
QY 88 LNEKSKOEELLKQNLQLEALORANFSGPCPODWIMHKENCYLF-HGPGMEKNQTC 146
DB 109 LDEKSKLMEHLRONLNLQEVLEKAAVSGPCPODWIMHEENCYQFSSGSFMEKESQENC 168
QY 147 QSLGGOLQINGADDLFTIILQAIHTTSPFVIGLHRRKPGCPWIMENGTPLNPFKTRG 206
DB 169 LSLDAHLKLNSTDELEFIQMIHASSPFWGLSMRKNYSWLMEGDTPLPHLFRIOG 228
QY 207 VSLQVSSNCAYLQDGAFAENCILIAFSICOKKTNHLQ 246
DB 229 AVSRMPSGTCAYIQRGTVFAENCILIAFSICOKKANILR 268

RESULT 7
US-08-809-494A-4
; Sequence 4, Application US/08809494A
; Patent No. 5962260
; GENERAL INFORMATION:
; APPLICANT: Sawamura, Tatsuya
; TITLE OF INVENTION: Modified Low-Density Lipoprotein
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAlay Fisher Nissen Goldberg & Kiel
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,494A
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-321705
; FILING DATE: 30-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-214206
; FILING DATE: 31-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldberg, Jules E
; REGISTRATION NUMBER: 24408
; REFERENCE/DOCKET NUMBER: JG-Y-4363PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 986-4090
; TELEFAX: 212 818-9479
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-494A-4

Query Match 45.1%; Score 594.5; DB 2; Length 273;
Best Local Similarity 44.2%; Pred. No. 9.9e-46;
Matches 125; Conservative 39; Mismatches 70; Indels 49; Gaps 6;

QY 1 MTFDDMKRPADEPDQKCGKKPK-----EE 26
D 1 MTFDDMKRPADEPDQKCGKKPK-----EE 26
QY 27 SORLEKGRIDITRRKLDKSKOEELL--OMIQNQLQALORANSSSORELKGKIDTL 84
D 1 MTFDDMKRPADEPDQKCGKKPK-----EE 26
QY 60 SQ-----VSDILKQOANTHEDILEGQIL-----AQRSEKSAQESQKELKEMITL 108
D 60 SQ-----VSDILKQOANTHEDILEGQIL-----AQRSEKSAQESQKELKEMITL 108
QY 85 TLKLNKSKOEELLQKQNLQALORANSSGPPQDMLMKENCYLTF-HGPFGEKRN 143
D 109 AHKLDKSKKLMELHRQNLNQLQALORANSSGPPQDMLMKENCYLTF-HGPFGEKRN 143
QY 144 QTCOSLQGLQIINGADLITFLQAIISHTSPFWIGLHKKRGQPLWENGTPPLNFQPFK 203
D 169 ENCLSLDHLKINSTDELEFIQOMIAHSSPFPMGLSMKRPNYSWLMWEDGTPPLPHLFR 228
QY 204 TRGVSLQYSSSNCAYLQDGAFAENCILITAFSIOCKTNHLO 246
D 229 IQGAVSRMTPSGTCAYIQRGIVFAENCILITAFSIOCKTNHLO 271

RESULT 8

US-09-352-302-4
Sequence 4, Application US/09352302
Patent No. 6197937
GENERAL INFORMATION:
APPLICANT: Sawamura, Tatsuya
APPLICANT: Masaki, Tomoo
TITLE OF INVENTION: Modified Low-Density Lipoprotein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAlay Fisher Nissen Goldberg & Kiel
STREET: 261 Madison Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/352.302
FILING DATE: 12-JUL-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-321705
FILING DATE: 30-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-214206
FILING DATE: 31-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Goldberg, Jules E
REGISTRATION NUMBER: 24408
REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 986-4090
TELEFAX: 212 818-9479
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-352-302-4

Query Match 45.1%; Score 594.5; DB 4; Length 273;
Best Local Similarity 44.2%; Pred. No. 9.9e-46;
Matches 125; Conservative 39; Mismatches 70; Indels 49; Gaps 6;

QY 1 MTFDDMKRPADEPDQKCGKKPK-----EE 26
D 1 MTFDDMKRPADEPDQKCGKKPK-----EE 26
QY 27 SORLEKGRIDITRRKLDKSKOEELL--OMIQNQLQALORANSSSORELKGKIDTL 84
D 1 MTFDDMKRPADEPDQKCGKKPK-----EE 26
QY 60 SQ-----VSDILKQOANTHEDILEGQIL-----AQRSEKSAQESQKELKEMITL 108
D 60 SQ-----VSDILKQOANTHEDILEGQIL-----AQRSEKSAQESQKELKEMITL 108
QY 85 TLKLNKSKOEELLQKQNLQALORANSSGPPQDMLMKENCYLTF-HGPFGEKRN 143
D 109 AHKLDKSKKLMELHRQNLNQLQALORANSSGPPQDMLMKENCYLTF-HGPFGEKRN 143
QY 144 QTCOSLQGLQIINGADLITFLQAIISHTSPFWIGLHKKRGQPLWENGTPPLNFQPFK 203
D 169 ENCLSLDHLKINSTDELEFIQOMIAHSSPFPMGLSMKRPNYSWLMWEDGTPPLPHLFR 228
QY 204 TRGVSLQYSSSNCAYLQDGAFAENCILITAFSIOCKTNHLO 246
D 229 IQGAVSRMTPSGTCAYIQRGIVFAENCILITAFSIOCKTNHLO 271

RESULT 9

US-08-688-342-1
Sequence 1, Application US/08688342
Patent No. 5871964
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Cocks, Benjamin G.
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/688.342
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: MMLRIDT01
CLONE: 515847
US-08-688-342-1

Query Match 19.0%; Score 251; DB 2; Length 201;
Best Local Similarity 35.2%; Pred. No. 3.7e-15;

APPLICANT: Arizumi, Kiyoshi
APPLICANT: Takashima, Akira
TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,440
FILING DATE: CONCURRENTLY HERewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTXD:493
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 176 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-772-440-8

Query Match 17.5%; Score 231; DB 3; Length 176;
Best Local Similarity 30.9%; Pred. No. 1.9e-13;
Matches 50; Conservative 27; Mismatches 83; Indels 2; Gaps 2;

Qy 82 DTLTLKLNKSKOEELLQKNOQLQALQRAANFSGPCPDWLMHKNCYLF-HGPFGE 140
Db 14 DNFLSRNKHNKPTSSIDEKVAPSKASQTGCGFSGCLPMIMHGKSCYLFSGNSWY 73
Qy 141 KNRQTCQSLGGLQINGADLTFT-LQAISSHTTSPFWIGLHRRKPGQWMLNENGTPLNF 199
Db 74 GSKRHCSQGLAHLKIDNSKEFEFTESQSSHRINAFWIGLSRNSQEGFWEDGSAPFP 133
Qy 200 OFFKTRGVSLQLYSSNCAYLQDGAFAENCILIAFSICOKK 241
Db 134 NSFQVRNTVPQESLHNCVWINGSEVYNGICNTSSISICEKE 175

RESULT 13
US-08-772-440-2
Sequence 2, Application US/08772440
Patent No. 6046158
GENERAL INFORMATION:
APPLICANT: Arizumi, Kiyoshi
APPLICANT: Takashima, Akira
TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,440
FILING DATE: CONCURRENTLY HERewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTXD:493
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-772-440-2

Query Match 17.5%; Score 231; DB 3; Length 244;
Best Local Similarity 30.9%; Pred. No. 3e-13;
Matches 50; Conservative 27; Mismatches 83; Indels 2; Gaps 2;

Qy 82 DTLTLKLNKSKOEELLQKNOQLQALQRAANFSGPCPDWLMHKNCYLF-HGPFGE 140
Db 82 DNFLSRNKHNKPTSSIDEKVAPSKASQTGCGFSGCLPMIMHGKSCYLFSGNSWY 141
Qy 141 KNRQTCQSLGGLQINGADLTFT-LQAISSHTTSPFWIGLHRRKPGQWMLNENGTPLNF 199
Db 142 GSKRHCSQGLAHLKIDNSKEFEFTESQSSHRINAFWIGLSRNSQEGFWEDGSAPFP 201
Qy 200 OFFKTRGVSLQLYSSNCAYLQDGAFAENCILIAFSICOKK 241
Db 202 NSFQVRNTVPQESLHNCVWINGSEVYNGICNTSSISICEKE 243

RESULT 14
US-09-055-095-1
Sequence 1, Application US/09055095
Patent No. 5945308
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Patterson, Chandra
APPLICANT: Corley, Neil C.
APPLICANT: Salter, Susan
TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/055,095
FILING DATE: Filed Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:

```
;
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0500 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 284 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGNOT09
; CLONE: 1355922
; US-09-055-095-1

Query Match      16.8%; Score 221; DB 2; Length 284;
Best Local Similarity 29.2%; Pred. No. 2.9e-12;
Matches 52; Conservative 34; Mismatches 72; Indels 20; Gaps 6;

Y      81 IDFTLKLNKSKOEELQKQNLQALQRAA-----NFSG-----PCQDDMLMHK 127
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     90 ISQMERLGTTSQELQSLQVQNTKLAGSLQHVAKELCRELYNKAGAHRCSPCTQOMKWHG 149
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY    128 ENCYLEFH-GPFGEKNRQTCQSLGQLQINGADDLTFIL-QAISHTTSPFWIGLHRRKP 185
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db    150 DMTYGFYKDSKSWEDCKYFELSENSTWLKINKQEDLEFASQSYSEFFYSYWTGLLRPDS 209
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY    186 GQPLWENGTPLNQFFKTRGVSLQLY--SSNCAYLQDGAVFAENCILIAFSICQK 241
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db    210 GKAMLMWDGTPFTSELFH--IIIDVTPSRSDCAVAILNGMIFSKDCELRKVCERR 264

RESULT 15
US-08-772-440-13
; Sequence 13, Application US/08772440
; Patent No. 6046158
; GENERAL INFORMATION:
; APPLICANT: Arizumi, Kiyoshi
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,440
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTXD:493
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
```

```
;
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-772-440-13

Query Match      16.2%; Score 214; DB 3; Length 199;
Best Local Similarity 33.3%; Pred. No. 7.6e-12;
Matches 43; Conservative 24; Mismatches 60; Indels 2; Gaps 2;

QY    115 FSGPCPDMLMHKENCYLEF-HGPFGEKNRQTCQSLGQLQINGADDLTFIL-QAISHTT 172
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db    70 FSGSCLEPNWIMHGKSCYLEFSGSGNSWYSGKRHCQSLGAHLKIDNSKEFFIESQTSR 129
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY    173 TSPFWIGLHRRKKGQPLWENGTPLNQFFKTRGVSLQLYSSNCAYLQDGAVFAENCIL 232
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db    130 INAFWIGLSRNQSEGPFWEEDGSAFFPNSTFOVRTVPOESLHNCAVIMHGEVYNOICNT 189
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY    233 IAFSICQK 241
Db    190 SSYSTCKE 198
```

Search completed: August 19, 2002, 22:58:04
Job time: 3395 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 19, 2002, 22:02:39 ; Search time 43.79 Seconds
(without alignments) 541.997 Million cell updates/sec

Title: US-09-898-554-14

Perfect score: 1319

Sequence: 1 MTFDDKMKRANDEPDQKSCG.....ENCILIAFSICKKTNHLQI 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.71.*

1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1207	91.5	363	2 JE0111	lectin-like oxidiz
2	223	16.9	404	2 A46274	HIV gp120-binding
3	222.5	16.9	223	2 B46467	NKR-p1 protein hom
4	218.5	16.6	220	2 C46467	NKR-p1 protein hom
5	201.5	15.3	227	2 A46467	natural killer cel
6	190	14.4	309	1 S34198	IgE Fc receptor II
7	187.5	14.2	156	2 T28141	C type lectin, B 1
8	186	14.1	331	1 LNMSFR	IgE Fc receptor, I
9	174	13.2	223	2 A35917	NK-cell receptor p
10	168.5	12.8	257	2 I50146	gene 17.5 protein
11	165.5	12.5	321	1 LNHDUR	IgE Fc receptor II
12	164.5	12.5	311	1 LNHDUR	asialoglycoprotein
13	163.5	12.4	550	2 A28166	Kufler cell recep
14	162.5	12.3	231	2 PR0374	natural killer cel
15	159	12.1	240	2 I54524	natural killer cel
16	159	12.1	1326	2 B56395	secretory phoshol
17	159	12.1	1465	2 A56395	secretory phoshol
18	158.5	12.0	216	2 PR0375	natural killer cel
19	156	11.8	265	2 I49050	Ly-49E-GE antigen
20	154.5	11.7	199	2 JH0822	lymphocyte early a
21	149.5	11.3	233	2 PR0372	natural killer cel
22	149	11.3	304	2 JX0209	lectin, galactose/
23	149	11.3	1479	2 T42710	mannose receptor,
24	148.5	11.3	225	2 I38700	hNKR-P1a protein -
25	142	10.8	1458	1 A49707	phospholipase A2 r
26	141.5	10.7	1463	2 A53210	phospholipase A2 r
27	137.5	10.4	1487	2 S48719	phospholipase A(2)
28	137	10.4	288	2 I49058	Ly49c - mouse
29	136.5	10.3	262	2 A45813	T-cell surface gly

30	135	10.2	266	2 I49059	Ly49c - mouse
31	131.5	10.0	266	2 I49363	natural killer cel
32	131.5	10.0	306	2 A42230	lectin M-ASGP-BP p
33	131	9.9	354	2 A32331	B-cell differentia
34	130.5	9.9	262	2 I49361	natural killer cel
35	130.5	9.9	291	1 LNHDUR	hepatic lectin H1
36	130.5	9.9	1455	1 A48925	mannose receptor p
37	130	9.9	266	2 I49114	Ly49H - mouse
38	129	9.8	552	2 C96563	probable protein k
39	128.5	9.7	262	2 A30573	T-cell surface gly
40	128	9.7	321	2 T26152	hypothetical prote
41	127.5	9.7	237	2 J07608	type II lectin-lik
42	127.5	9.7	1456	1 A36563	mannose receptor p
43	127	9.6	359	2 A46509	B cell differentia
44	126	9.6	167	1 MNVZP2	hepatic lectin hom
45	125.5	9.5	301	2 S13165	asialoglycoprotein

ALIGNMENTS

RESULT 1

JE0111 Lectin-like oxidized LDL receptor - mouse

N:Alternate names: LDY-1

C:Species: Mus musculus (house mouse)

C:Date: 22-May-1998 #sequence_revision 29-May-1998 #text_change 07-May-1999

C:Accession: JE0111

R:Hoshikawa, H.; Sawamura, T.; Kakutani, M.; Aoyama, T.; Nakamura, T.; Masaki, T.

Biochem. Biophys. Res. Commun. 245, 841-846, 1998

A:Title: High affinity binding of oxidized LDL to mouse lectin-like oxidized LDL rece

A:Reference number: JE0111; MUID:98249801

A:Accession: JE0111

A:Molecule type: mRNA

A:Residues: 1-363 <HOS>

F:34-59/Domain: transmembrane #status predicted <TM>

Query Match 91.5% Score 1207; DB 2; Length 363;

Best Local Similarity 66.1%; Pred. No. 4, 1e-71;

Matches 240; Conservative 1; Mismatches 6; Indels 116; Gaps 1;

QY	1	MTFDDKMKRANDEPDQKSCGKKPK	-----	24
DB	1	MTFDDKMKRANDEPDQKSCGKKPKGLHLLSPWPFRAATVILCLVLSVTLLVQGTQLR	60	
QY	25	-----	24	
DB	61	QVSDLLKQYANLTOODRILEGOMLAQCKAENTSOESKKELGKIDTLTQKINKEKQOE	120	
QY	25	-----	64	
DB	121	ELLQKNQNLQELALORANSEESQRELKGIIDTLTKLDEKSEDELLQMTQNLQELALQ	180	
QY	65	RAANSEESQRELKGIIDTLTKLNEKSEQELQKNQNLQELALORANFSGPCQDML	124	
DB	181	RAANSEESQFELKGIIDTLTKLNEKSEQELQKNQNLQELALORANFSGPCQDML	240	
QY	125	WIKENCYLFHGGPGWEKNQTCOSLGGQLQINGADLTFILQAISSHSPWIGLHRRK	184	
DB	241	WIKENCYLFHGGPGWEKNQTCOSLGGQLQINGADLTFILQAISSHSPWIGLHRRK	300	
QY	185	POCPWMEGTPLNQFFETRGVSLQYSSNCAYLQDGAFAENCILIAFSICKKTNH	244	
DB	301	POCPWMEGTPLNQFFETRGVSLQYSSNCAYLQDGAFAENCILIAFSICKKTNH	360	
QY	245	LQI 247		
DB	361	LQI 363		
RESULT	2			
		A46274		

HIV gp120-binding C-type lectin - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-1995
C:Accession: A46274
R:Curis, B.M.; Scharnowske, S.; Watson, A.J.
Proc. Natl. Acad. Sci. U.S.A. 89, 8356-8360, 1992
A:Title: Sequence and expression of a membrane-associated C-type lectin that exhibits C
A:Reference number: A46274; MUID:92390446
A:Accession: A46274
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-404 <CUR>
A:Experimental source: placenta
A:Note: sequence extracted from NCBI backbone (NCBIN:113134, NCBIP:113135)
C:Superfamily: C-type lectin homology
F:256-377/Domain: C-type lectin homology <LCH>

Query Match 16.9%; Score 223; DB 2; Length 404;
Best Local Similarity 26.0%; Pred. No. 2,1e-07;
Matches 67; Conservative 54; Mismatches 107; Indels 30; Gaps 10;

Y 6 MKRPANDEPOK-----CGKRPRESQRELKGIIDTIT--TRKLDKSK 47
Db 129 RLKAAYGELEPKSKQEIYELTLKRAAYGELEPKSKQEIYELTLKRAAYGELEPKSK 188
QY 48 EDELLQMIQNLQELQRAANSEESQ--RELKGIIDTLTLKLNKSEDELLQKQNL 105
Db 189 -QOEIYELTLKRAAYGELEPKSKQEIYELTLKRAAYGELEPKSK -QOEIYELTLQ 245
QY 106 QELQRAANSGPCPDWLMHKENCY-LFHGPGWCKNRTQCSGLQIQNCADLT 164
Db 246 KAAVERICH--PCPMEWTFEGNCFYMSQRMWHDITACKEVGAQLVYISAEQNF 302
QY 165 ILQAIISHTTSPFWIGLHRRKPGQPMLENGTPL--NFQFKTRGVSLQLYSSNCAYLQD 222
Db 303 LQLOSSNSNFTWGLSDLNQEGTWQVDSPLLPSTKQYWNKGPNNV--GEEDCAFEFG 361
QY 223 GAVFAENCILIAFSICOK 240
Db 362 NGWMDCKNLAKFWICK 379

RESULT 3
B46467
NKR-P1 protein homolog - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999
C:Accession: B46467
R:Giorda, R.; Trucco, M.
Immunol. 147, 1701-1708, 1991
A:Title: A family of genes selectively coexpressed in adherent lymphokine-activated kill
A:Reference number: A46467; MUID:91349596
A:Accession: B46467
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-223 <GIO>
A:Cross-references: GB:M77677; NID:q200060; PIDN:AAA39823.1; PID:q200061
A:Experimental source: NK cells, C57BL/7
A:Note: sequence extracted from NCBI backbone (NCBIN:52380, NCBIP:52381)
C:Superfamily: natural killer cell receptor p1; C-type lectin homology
C:Keywords: transmembrane protein
F:94-210/Domain: C-type lectin homology <LCH>

Query Match 16.9%; Score 222.5; DB 2; Length 223;
Best Local Similarity 32.1%; Pred. No. 1.2e-07;
Matches 50; Conservative 22; Mismatches 77; Indels 7; Gaps 3;

QY 90 EKSKQDELLQKQNLQELQRAANSGPCPDWLMHKENCY-LFHGPGWCKNRTQCS 148
Db 67 QKSSVQKICADVQENRHTTDCSVNLE--CPQDWLSHRDCFRNFQVSNWESQADCGR 124

QY 149 LGQQLQINGADLTFLQAIISHTTSPFWIGLHRRKPGQPMLENGTPLNFQFKTRGV 208
Db 125 KGATLLIQDEELRFLDLSIKENYFNWIGLRFPTLPDMWKNWINGTFNSDYLIGDT 184
QY 209 LQIYSSNCAYLQDGAFAENCILIAFSICOKKTNH 244
Db 185 ----ENGSCASISGDKVTSCTDNRMWICKKELNH 216

RESULT 4
C46467
NKR-P1 protein homolog gene-40 - mouse
N:Alternate names: natural killer cell activation molecule; NK1.1 alloantigen
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999
C:Accession: C46467; A46499
R:Giorda, R.; Trucco, M.
Immunol. 147, 1701-1708, 1991
A:Title: A family of genes selectively coexpressed in adherent lymphokine-activated k
A:Reference number: A46467; MUID:91349596
A:Accession: C46467
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-220 <GIO>
A:Cross-references: GB:M77678; NID:q200062; PIDN:AAA39824.1; PID:q200063
A:Experimental source: NK cells, C57BL/7
A:Note: sequence extracted from NCBI backbone (NCBIN:52382, NCBIP:52383)
R:Ryan, J.C.; Turk, J.; Nleml, E.C.; Yokoyama, W.M.; Seaman, W.E.
Immunol. 149, 1631-1635, 1992
A:Title: Molecular cloning of the NK1.1 antigen, a member of the NKR-P1 family of nat
A:Reference number: A46499; MUID:92373004
A:Accession: A46499
A:Molecule type: mRNA
A:Status: preliminary
A:Residues: 1-86, 90-220 <RYA>
A:Cross-references: GB:S43141; NID:q254094; PIDN:AAB22979.1; PID:q254095
A:Experimental source: C57BL/6J NK cells
A:Note: sequence extracted from NCBI backbone (NCBIN:111622, NCBIP:111624)
C:Superfamily: natural killer cell receptor p1; C-type lectin homology
C:Keywords: transmembrane protein
F:91-207/Domain: C-type lectin homology <LCH>

Query Match 16.6%; Score 218.5; DB 2; Length 220;
Best Local Similarity 33.1%; Pred. No. 2.2e-07;
Matches 50; Conservative 19; Mismatches 65; Indels 17; Gaps 3;

QY 95 OEELLQKQNLQELQRAANSGPCPDWLMHKENCY-LFHGPGWCKNRTQCSLGOL 153
Db 79 QENLQKTTVNDL-----CPQDWLHRRKCFHVSQVSNWTEGGQDCCRGATL 126
QY 154 LOINGADLTFLQAIISHTTSPFWIGLHRRKPGQPMLENGTPLNFQFKTRGVSLQLYS 213
Db 127 LLIQDQELRFLDLSIKENYFNWIGLRFPTLPDMWKNWINGTFNSDYLIGDT----E 182
QY 214 SSMCAVYLDGAVFAENCILIAFSICOKKTNH 244
Db 183 NGSCASILGDKVTPESCASDNRMWICKKELNH 213

RESULT 5
A46467
natural killer cell receptor p1 - mouse
N:Alternate names: NKR-P1 protein
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 19-Feb-1999 #text_change 05-May-2000
C:Accession: A46467; A46502; A46456
R:Giorda, R.; Trucco, M.
Immunol. 147, 1701-1708, 1991
A:Title: A family of genes selectively coexpressed in adherent lymphokine-activated k
A:Reference number: A46467; MUID:91349596
A:Accession: A46467
A:Molecule type: mRNA

A:Residues: 'MHLCT', 1-227 <GIO>
 A:Cross-references: GB:M77676; NID:9200058
 A:Experimental source: A-Irk cells, C57BL
 A:Note: sequence extracted from NCBI backbone (NCBIN:52378, NCBI:52379); the sequence
 R:Giorde, R., Weisberg, E.P., ID, T.K.; Trucco, M.
 J:Immunol. 149, 1957-1963, 1992
 A:Title: Genomic structure and strain-specific expression of the natural killer cell re
 A:Reference number: A46502; MUID:92388663
 A:Accession: A46502
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-109, 'H', 111-181, 'D', 183-227 <G12>
 A:Cross-references: GB:X64716; NID:953395; PIDN:CAA5971.1; PID:9817989
 A:Experimental source: BALB/c 3T3 fibroblastoid cell line
 A:Note: sequence extracted from NCBI backbone (NCBIN:113037, NCBIN:113063, NCBIN:113072,
 R:Yokoyama, W.M.; Ryan, J.C.; Hunter, J.J.; Smith, H.R.; Stark, M.; Seaman, W.E.
 J:Immunol. 147, 3228-3236, 1991
 A:Title: cDNA cloning of mouse NK-RP1 and genetic linkage with LY-49. Identification of
 A:Reference number: A46456; MUID:92013158
 A:Accession: A46456
 A:Molecule type: mRNA
 A:Residues: 1-38, 'L', 40-227 <YOK>
 A:Cross-references: GB:M77753; NID:918569; PIDN:AAA39366.1; PID:918570
 A:Note: sequence extracted from NCBI backbone (NCBIN:60429, NCBI:60431)
 C:Superfamily: natural killer cell receptor P1; C-type lectin homology
 F:94-210/Domain: C-type lectin homology <LCH>

Query Match 15.3%; Score 201.5; DB 2; Length 227;
 Best Local Similarity 32.2%; Pred. No. 2.8e-06;
 Matches 46; Conservative 21; Mismatches 69; Indels 7; Gaps 3;

OY 105 LOEALQRRANFSG--PCQODMLMHEKNCY-LFHGFGMEKNRQTCQSLGGLQINGADD 161
 Db 78 IQENLNKTTDCSAKIEQDMLSHDKCFHVSQVNTBEGLVDCDGGATMLIQDDE 137
 OY 162 LTFILQAISSHTSPFVIGLHRRKPGQPMWENGTPLNQFRTKRGVSLQLYSSNCAYLQ 221
 Db 138 LRFLLDSIKERYNSFWIGLRYTLPLDMNWKWINGSTLNSDVLKITDGT----ENDSCAIS 193
 OY 222 DGAVFAENCILAFSICCKKTNH 244
 Db 194 GDKVTFESCNSDMRWICCKELVH 216

RESULT 6
 634198
 A:Fc receptor II, low-affinity - rat
 N:Alternate names: CD23; lymphocyte Ige receptor
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 22-Jun-1999
 C:Accession: S34198
 R:Flores-Romo, L.; Sheld, J.; Humbert, Y.; Graber, P.; Aubry, J.P.; Gauchat, J.F.; Ayat
 submitted to the EMBL Data Library, June 1993
 A:Description: Inhibition of an in vivo antigen-specific Ige response by antibodies to C
 A:Reference number: S34198
 A:Accession: S34198
 A:Molecule type: mRNA
 A:Residues: 1-309 <FLO>
 A:Cross-references: EMBL:X73579; NID:9313672; PIDN:CAA51981.1; PID:9313673
 C:Superfamily: Ige receptor II; C-type lectin homology
 C:Keywords: B-cell; glycoprotein; immunoglobulin receptor; macrophage; tandem repeat; tr
 F:1-25/Domain: intracellular #status predicted <INT>
 F:14-22/Region: stop-transfer sequence
 F:24-46/Domain: transmembrane #status predicted <TM>
 F:47-309/Domain: extracellular #status predicted <EXT>
 F:126-309/Product: soluble Ige-binding factor (29K) #status predicted <IGI>
 F:149-309/Product: soluble Ige-binding factor (25-27K) #status predicted <BEF1>
 F:164-283/Domain: C-type lectin homology <LCH>
 F:192-283,260-274/Disulfide bonds: #status predicted

Query Match 14.4%; Score 190; DB 1; Length 309;

Best Local Similarity 24.8%; Pred. No. 2.2e-05;
 Matches 69; Conservative 42; Mismatches 85; Indels 82; Gaps 11;
 OY 13 EPPDQSCGKKKPREESORELTKIDITTRKL-----DKSKEO-----ELLQMI 56
 Db 11 EPPRRRC-CCARGTQLYVGLTTVMWLLALLLHWETKSLKQJADAATQNALQMS 69
 OY 57 QNLQALQRAANSSESORELKGIIDTFLKLNESK-----QOELLQKQNLQBAL 109
 Db 70 QNLDEL-----QAEQKQMSQDSQSLQNLNELQEDLQNKQNSLSQNLNTLQEDL 121
 OY 110 -----QRAANS-----GPCQDMLMHEKNCYL-FH 135
 Db 122 VVKSQGLNEKRAASDSLEKLEEVAKLWELMSKGTACNCPKDWLHFOQCYFEG 181
 OY 136 PFGMEKNRQTCQSLGGLQINGADDLTFILQAISSHTSPFVIGLHRRKPGQPMWENG 195
 Db 182 SKWQIAKFTCSDLGRVLSHSOKEDPLMOKINKES--WIGLQDLNMEGEFVWPGDS 239
 OY 196 PLNFOFKTRGVSLQLYSSNCAYLQDGAFAENCILI 233
 Db 240 PVG-----YSNMNPGEPNNGQ-GEDEVMA 263

RESULT 7
 T28141
 C type lectin, B locus - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T28141
 R:Milne, S.; Kaufman, J.; Beck, S.
 submitted to the EMBL Data Library, May 1998
 A:Description: DNA sequencing and analysis of the chicken major histocompatibility co
 A:Reference number: 220475
 A:Accession: T28141
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-156 <ML>
 A:Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292545; PIDN:CAA18961.1
 A:Experimental source: clone cB12
 C:Genetics: Blec
 A:Gene: Blec
 A:Map position: 16
 A:Introns: 17/1; 74/3; 110/2

Query Match 14.2%; Score 187.5; DB 2; Length 156;
 Best Local Similarity 30.9%; Pred. No. 1.5e-05;
 Matches 38; Conservative 20; Mismatches 54; Indels 11; Gaps 3;

OY 119 CPQDMLMHEKNCYL-FHGFMEKNRQTCQSLGGLQINGADDLTFILQAISSHTSPW 177
 Db 30 CPFDIGFRGKRYTSEDSNNTSSONNCASALGASLAFVDSKEDLSFTWR--HKSSPPW 87
 OY 178 IGLHRRKPGQPMWENGTPLNQFRTKRGVSLQLYSSNCAYLQDGAFAENCILAFSI 237
 Db 88 VGLSREGKHPWEWNRPSLSLFL-----QVGGDGLCAVLGAGLSSSCSRRMVY 139
 OY 238 COK 240
 Db 140 CTK 142

RESULT 8
 LMSER
 Ige Fc receptor, low-affinity - mouse
 N:Alternate names: Blast-2; CD23; Fc-epsilon-RII; lymphocyte Ige receptor
 C:Species: Mus musculus (house mouse)
 C:Date: 12-Feb-1993 #sequence_revision 28-Oct-1994 #text_change 22-Jun-1999
 C:Accession: A43518; A33840
 R:Gollnick, S.O.; Tronstine, M.L.; Yamashita, L.C.; Kehry, M.R.; Moore, K.W.
 J:Immunol. 144, 1974-1982, 1990
 A:Title: Isolation, characterization, and expression of cDNA clones encoding the mous

A:Molecule type: DNA
A:Residues: 157-284 <SUT>
A:Cross-references: GB:X06049; NID:931316
A:Note: all exon sequences were determined but the complete sequence is not shown
R:Matsumi, M.; Nunez, R.; Sachl, Y.; Lynch, R.G.; Yodoi, J.
FEBS Lett. 335, 51-56, 1993
A:Title: Alternative transcripts of the human CD23/Fc-epsilon-RII. A possible novel mechanism
A:Reference number: S39442; MUID:94063078
A:Accession: S39442
A:Molecule type: DNA
A:Residues: 1-7, 'D', 47-50 <MAS1>
A:Experimental source: splice form 'a'
A:Accession: S39443
A:Molecule type: DNA
A:Residues: 'NMPSOD', 47-50 <MAS2>
A:Experimental source: splice form 'b'
R:Ludin, C.; Hofstetter, H.; Sarfati, M.; Levy, C.A.; Suter, U.; Alaimo, D.; Kilcherr, EMO J. 6, 109-114, 1987
A:Title: Cloning and expression of the cDNA coding for a human lymphocyte IgE receptor.
A:Reference number: A26164; MUID:87218454
A:Accession: A26164
A:Molecule type: mRNA
A:Residues: 1-268, 'T', 270-321 <LUD>
A:Cross-references: GB:X04772; NID:934002; PIDN:CAA28465.1; PID:934003
A:Note: the codon given for 269-Asn (ACC) is inconsistent with the authors' translation
A:Note: part of this sequence, including the amino end of soluble forms of the protein,
R:Ikuta, K.; Takami, M.; Kim, C.W.; Honjo, T.; Miyoshi, T.; Tagaya, Y.; Kawabe, T.; Yodoi Proc. Natl. Acad. Sci. U.S.A. 84, 819-823, 1987
A:Title: Human lymphocyte Fc receptor for IgE: sequence homology of its cloned cDNA with
A:Reference number: A26589; MUID:87118255
A:Accession: A26589
A:Molecule type: mRNA
A:Residues: 1-321 <IRU>
A:Cross-references: GB:M15059; NID:9182447; PIDN:AAA52434.1; PID:9182448
A:Note: part of this sequence, including the amino end of soluble forms of the protein,
R:Yokota, A.; Kikuchi, H.; Tanaka, T.; Sato, R.; Barsumian, E.L.; Suenmura, M.; Kishimoto Cell 55, 611-618, 1988
A:Title: Two species of human Fc-epsilon receptor II (Fc-epsilon-RII/CD23): tissue-specific
A:Reference number: A31924; MUID:89028672
A:Accession: A31924
A:Molecule type: mRNA
A:Residues: 'NMPSO', 8-14 <YOK>
A:Cross-references: GB:M23562; NID:9182444
A:Experimental source: splice form IIB
R:Letellier, M.; Sarfati, M.; Delespesse, G.
Mol. Immunol. 26, 1105-1112, 1989
A:Title: Mechanisms of formation of IgE-binding factors (soluble CD23)-I. Fc epsilon R II
A:Reference number: JLO132; MUID:90220658
A:Accession: JLO132
A:Molecule type: protein
A:Residues: 1-321 <LET>
A:Experimental source: lymphoblastoid B cell line
R:Rose, K.; Nutcull, G.; Graber, P.; Pochon, S.; Regamey, P.O.; Jansen, K.U.; Magnenat, Biochem. J. 286, 819-824, 1992
A:Title: Partial characterization of natural and recombinant human soluble CD23.
A:Reference number: S29107; MUID:93038513
A:Accession: S29107
A:Molecule type: protein
A:Residues: 152-166, 173-179, 189-212, 230-263, 268-306 <ROS>
R:Padlan, E.A.; Helm, B.A.
submitted to the Brookhaven Protein Data Bank, June 1993
A:Reference number: A51791; PDB:1HLI
A:Contents: annotation; conformation by theoretical model, residues 173-285
R:Bejorath, J.
submitted to the Brookhaven Protein Data Bank, November 1995
A:Reference number: A65963; PDB:1KUE
A:Contents: annotation; conformation by theoretical model, residues 173-285
C:Comment: The sequence of the splice form 'a' is shown.
C:Comment: This receptor for the Fc portion of IgE is expressed in various hematopoietic cells.
C:Comment: Splice form 'a' is expressed constitutively in B-cells; 'b' is expressed in other cells.
C:Comment: Soluble IgE-binding factors are produced by proteolytic cleavage of IgE Fc region.
C:Genetics:

A:Gene: GDB:FCER2; FCE2
A:Cross-references: GDB:118888; OMIM:151445
A:Map position: 19p13.3-19p13.3
A:Introns: 8/1, 46/1, 64/1, 85/1, 106/1, 127/1, 157/1, 207/3, 243/2
C:Superfamily: IgE receptor II; C-type lectin homology
C:Keywords: alternative splicing; B-cell; glycoprotein; immunoglobulin receptor; macrophage; 'NMPSOD', 47-321/Product; IgE Fc receptor II, splice form b' #status predicted <SRB>
F: 'NMPSO', 8-321/Product; IgE Fc receptor II, splice form b #status predicted <SRB>
F:1-321/Product; IgE Fc receptor II, splice form a #status predicted <SFA>
F:1-23/DNA; Intracellular #status predicted <INT>
F:1-7, 'D', 47-321/Product; IgE Fc receptor II, splice form 'a' #status predicted <SFA>
F:14-20/Region: stop-transfer sequence
F:22-45/DNA; transmembrane #status predicted <TM>
F:46-321/DNA; extracellular #status predicted <EXT>
F:64-84/Region: 21-residue repeat
F:81-321/Product; soluble IgE-binding factor (37K) #status predicted <IG>
F:85-105/Region: 21-residue repeat
F:102-321/Product; soluble IgE-binding factor (33K) #status predicted <IGB>
F:106-126/Region: 21-residue repeat
F:125-321/Product; soluble IgE-binding factor (29K) #status predicted <IGT>
F:148-321/Product; soluble IgE-binding factor (25-27K), long form #status experimental
F:150-321/Product; soluble IgE-binding factor (25-27K), short form #status experimental
F:163-282/DNA; C-type lectin homology <LCH>
F:63/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:147-148/Cleavage site: Lys-Ileu (unidentified proteinase) #status experimental
F:149-150/Cleavage site: Arg-Ileu (unidentified proteinase) #status experimental
F:191-282, 259-273/Disulfide bonds: #status experimental

Query Match 12.5%; Score 165.5; DB 1; Length 321;
Best Local Similarity 28.7%; Pred. No. 0.00087;
Matches 51; Conservative 33; Mismatches 75; Indels 19; Gaps 7;

QY 28 QRELKGIKIDITTRKDEKDEEL---LQNTQNLQALQRAANSSEBSQELKGIKIDT 83
DB 78 QMAQKSSQTSQSELEELAEQRLKSDLELSWNL-NLQ--ADLSFKSQELER--- 131
QY 84 LFLKLNKSKQDEELQNLQALQRAANF-SGPCPDQMLHMKENCLF-HGPFQWPK 141
DB 132 -----NEASDLLERLREETTKLRLMELQVSSGCVCTPCPKTFNFRCKYFGKKQWVH 186
QY 142 NRQTCOSLQGLQINGADLFLILQALSHTPSPWIGLHRKPKQPMWENGTPLPNF 199
DB 187 ARVACDDMDGQVLSHSPEQDFLRKHSHTGS--WIGLRNLDLGEFLWVGSHVDY 242

RESULT 12
LNH02A
asialoglycoprotein receptor H2a - human
N:Alternate names: hepatic lectin H2a
N:Contents: ASGPR; asialoglycoprotein receptor H2a; asialoglycoprotein receptor H2b
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text change 10-Dec-1999
C:Accession: A25179; A39100; B39100; I37995; A49466; B49466; S14525
R:Spies, M.; Lodish, H.F.
Proc. Natl. Acad. Sci. U.S.A. 82, 6465-6469, 1985
A:Title: Sequence of a second human asialoglycoprotein receptor: conservation of two
A:Reference number: A25179; MUID:86016723
A:Accession: A25179
A:Molecule type: mRNA
A:Residues: 1-311 <SPI>
A:Cross-references: GB:M11025; NID:9179080; PIDN:AA59519.1; PID:9179081
R:Leiderkramer, G.Z.; Lodish, H.F.
J. Biol. Chem. 266, 1237-1244, 1991
A:Title: An alternatively spliced minilexon alters the subcellular fate of the human a
A:Reference number: A39100; MUID:91093236
A:Accession: A39100
A:Molecule type: DNA
A:Residues: 69-99 <LED>
A:Cross-references: GB:M38420; NID:9184395
A:Accession: B39100
A:Molecule type: DNA; mRNA

A;Residues: 69-81,87-99 <LE2>
A;Cross-references: GB:M38420; NID:g184395
R;Paletta, E.; Stockert, R.J.; Racevskis, J.
Hepatology 15, 395-402, 1992
A;Title: Differences in the abundance of variably spliced transcripts for the second asialo
A;Reference number: I37995; MUID:92184202
A;Accession: I37995
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-23,43-81,87-311 <PAI>
A;Cross-references: EMBL:X55283; NID:g34354; PIDN:CAA38997.1; PID:g34355
R;Yuk, M.H.; Lodish, H.F.
J. Cell Biol. 123, 1735-1749, 1993
A;Title: Two pathways for the degradation of the H2 subunit of the asialoglycoprotein re
A;Reference number: A49466; MUID:94103329
A;Accession: A49466
A;Molecule type: protein
A;Residues: 78-98 <YUK>
A;Accession: B49466
A;Molecule type: protein
A;Residues: 87-98 <YU2>
A;Comment: The functioning ligand-binding unit of this receptor is thought to be at least
A;Genetics:
A;Gene: GDB:ASGR2; L-H2
A;Cross-references: GDB:118755; OMIM:108361
A;Map position: 17p13-17p11
C;Superfamily: hepatic lectin; C-type lectin homology
C;Keywords: alternative splicing; endocytosis; glycoprotein; lectin; liver; phosphoprote
F;1-311/Product: asialoglycoprotein receptor H2a #status predicted <MNT1>
F;1-81,87-311/Product: asialoglycoprotein receptor H2b #status predicted <MAT2>
F;1-58/Domain: intracellular #status predicted <INT>
F;1-23,43-81,87-311/Product: asialoglycoprotein receptor H2c #status predicted <MAT3>
F;59-78/Domain: transmembrane #status predicted <TM>
F;79-311/Domain: extracellular #status predicted <EXT>
F;177-300/Domain: C-type lectin homology <LCH>
F;102,170,305/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.5%; Score 164.5; DB 1; Length 311;
Best Local Similarity 25.1%; Pred. No. 0.00098;
Matches 59; Conservative 36; Mismatches 81; Indels 59; Gaps 11;

QY 51 ELQMIONLOEALORANSS-----ESSORELKKITPTLT 85
DB 88 QLOAELSLKEAFSNFSSSTLTVEQAISTHGSGYDKITSLGAKLEKQODLKADHDALL 147
QY 86 LKINKESE-----QELLQKNONLOEALORANFSGPCPDWLMHKEKCYLF-HGPF 138
DB 148 FHLKHFVVDLRFVACQKELLHNSG-----QRTG-----CPVNVHEHSGCYWFSHSGKA 197
QY 139 WEKNROTQSGQLGQQLQINGADLTFLQAIISHTTSPF--WIGLHRRKPGQPMWENGTP 196
DB 198 WAAAEKKYQOLENHLVYINWMEQKFIYQ--HTNPFNTWIGL--TDSGSMKWVGDGT 251
QY 197 LNFQEFKTRGVSL-----QIVSSSMCAVLO--DGAVFANCIILASISDOKKN 243
DB 252 YRHN-YKNMAVTPDPMHGHGSEDCVEYDPGRWNDDFLQVRYWVCEKRN 305

RESULT 13
A28166
Kupffer cell receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 05-Nov-1999
C;Accession: A38674; A28166
R;Hoyle, G.W.; Hill, R.L.
J. Biol. Chem. 266, 1850-1857, 1991
A;Title: Structure of the gene for a carbohydrate-binding receptor unique to rat Kupffer
A;Reference number: A38674; MUID:91107689
A;Accession: A38674
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-550 <HO2>

A;Cross-references: GB:M55532; NID:g203362; PIDN:AAA40892.1; PID:g203363
R;Hoyle, G.W.; Hill, R.L.
J. Biol. Chem. 263, 7487-7492, 1988
A;Title: Molecular cloning and sequencing of a cDNA for a carbohydrate binding recept
A;Reference number: A28166; MUID:88227939
A;Accession: A28166
A;Molecule type: mRNA
A;Residues: 1-550 <HOY>
A;Cross-references: GB:J03734; NID:g205050; PIDN:AAA41472.1; PID:g205051
C;Superfamily: C-type lectin homology
C;Keywords: transmembrane protein
F;412-536/Domain: C-type lectin homology <LCH>

Query Match 12.4%; Score 163.5; DB 2; Length 550;
Best Local Similarity 22.8%; Pred. No. 0.0021;
Matches 62; Conservative 55; Mismatches 112; Indels 43; Gaps 12;

QY 2 TFDDKMKPAN--DEPDQSCGKKPKREORELKGKIDITTRKIDKSKOEELQMIQN 58
DB 283 TLTAQIONANGHLEQDTPTQLOGLKAQLKSTSLNSQIEVVGKLDSSRELTQLRDLSD 342
QY 59 LQELORAANSSEORELKGKIDTLTLKLNKSKOEELQKNONLOEALOR--AANFS 116
DB 343 V-SALKSNVOMLOSNLOKAAEVOSLKTGL-EATYTLAAKIQGOQSDLEALQKVAANTQ 400
QY 117 GP-----CPQDWLMHKEKCYLF-HGPFGEKNROTQSLGQQLQINGADLTFL 166
DB 401 GQKQNOVLQIMDMKMYFNKGFYFERSDKMSHEANFCVSGAHLASVTSQEQAFIV 460
QY 167 Q---AIGHTTSPFVGLHRRKPGQPMWENGTPLNFOFFKTRGVSLQIVSSNCAYIQDG 223
DB 461 QITNAVPH-----WIGLDGTGECNMRWVGDGP--FDYVOSR--RFRKRGQPDNMRHG 509
QY 224 AVFAENCILF-----AFS-ICOQKTN 243
DB 510 NGEREDCVHILORMMNDACGTAYVWVCKKSTD 541

RESULT 14
PT0374
Natural killer cell receptor group 2-C, splice form 1 - human
N;Alternate names: NKG-C
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 19-May-2000
C;Accession: PT0374
R;Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.
J. Exp. Med. 173, 1017-1020, 1991
A;Title: DNA sequence analysis of NKG2, a family of related cDNA clones encoding type
A;Reference number: PT0372; MUID:91178434
A;Accession: PT0374
A;Molecule type: mRNA
A;Residues: 1-231 <HOU>
A;Cross-references: EMBL:X54869; NID:g35060; PIDN:CAA38651.1; PID:g35061
A;Experimental source: natural killer cell
C;Genetics:
A;Gene: GDB:KLRC2; NKG2-C
A;Cross-references: GDB:9787095
A;Map position: 12p13-12p13
C;Superfamily: natural killer cell receptor PI; C-type lectin homology
C;Keywords: glycoprotein; transmembrane protein
F;71-96/Domain: transmembrane #status predicted <TRA>
F;27,100,149,178/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.3%; Score 162.5; DB 2; Length 231;
Best Local Similarity 23.0%; Pred. No. 0.00096;
Matches 53; Conservative 37; Mismatches 101; Indels 39; Gaps 7;

QY 18 SCGKKPKESQRELKGIIDITTRKIDKSKOEELQMIQNLQEA-----LOR 65
DB 12 SLADPKRKQ-QRKPKKSSI-----SGTDEIRPYVELNLQNPINHGQIDKITYDCG 63

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August, 19, 2002, 22:58:09 ; Search time 24.97 seconds
(without alignments)
383.009 Million cell updates/sec

Title: US-09-898-554-14

Perfect score: 1319

Sequence: 1 MFPEDKMKRANDEPDQKSCG.....ENCILAFSICQKKNHLOI 247

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	222.5	16.9	223	1	NK12_MOUSE
2	218.5	16.6	220	1	NK14_MOUSE
3	201.5	15.3	227	1	NK11_MOUSE
4	186	14.1	331	1	PCSE2_MOUSE
5	174	13.2	223	1	NK13_RAT
6	166	12.6	179	1	CD94_HUMAN
7	165.5	12.5	321	1	PCSE2_HUMAN
8	164.5	12.5	311	1	LECI_HUMAN
9	163.5	12.4	550	1	KUCR_RAT
10	162.5	12.3	231	1	NKGC_HUMAN
11	160.5	12.2	548	1	KUCR_MOUSE
12	159	12.1	240	1	NKGE_HUMAN
13	158.5	12.0	216	1	NKGD_HUMAN
14	156	11.8	266	1	KLR5_MOUSE
15	154.5	11.7	199	1	CD69_HUMAN
16	149.5	11.3	233	1	NKGA_HUMAN
17	149	11.3	304	1	MMGL_MOUSE
18	142	10.8	1458	1	PA2R_RABIT
19	141.5	10.7	1463	1	PA2R_BOVIN
20	137	10.4	288	1	KLR2_MOUSE
21	135	10.2	266	1	KLR3_MOUSE
22	133.5	10.1	149	1	CLF2_HUMAN
23	133	10.1	199	1	CD69_MOUSE
24	131.5	10.0	306	1	MMGL_RAT
25	131	9.9	354	1	CD72_MOUSE
26	130.5	9.9	290	1	LECH_HUMAN
27	130	9.9	266	1	KLR8_MOUSE
28	128.5	9.7	163	1	V239_FOWPY
29	128.5	9.7	262	1	LY4A_HUMAN
30	127.5	9.7	1456	1	MANR_HUMAN
31	126	9.6	167	1	V008_FOWPY
32	125.5	9.5	301	1	LECI_MOUSE
33	124.5	9.4	1019	1	LECI_TACTR

ALIGNMENTS

34	122.5	9.3	1019	1	LFC_CARRO	Q26422 carcinoscor
35	122	9.2	266	1	KLR6_MOUSE	O60653 mus musculu
36	119.5	9.1	2116	1	MYS2_DICDI	P08799 dictyosteli
37	119	9.0	146	1	IXB_TRIFL	P23807 trimeresuru
38	119	9.0	1203	1	XCPE_XENLA	P50533 xenopus lae
39	117.5	8.9	359	1	CD72_HUMAN	P34927 mus musculu
40	115	8.7	283	1	LECH_MOUSE	O60651 mus musculu
41	114.5	8.7	263	1	KLR4_MOUSE	O01758 osmerus mor
42	113.5	8.6	175	1	ANP_OSMO	P05140 hemipter
43	111	8.4	163	1	ANP_HEMAM	P02707 gallus gall
44	111	8.4	207	1	LECH_CHICK	O35594 mus musculu
45	111	8.4	414	1	CDV1_MOUSE	

RESULT 1						
ID	NK12_MOUSE	STANDARD:	PRT:	223	AA.	
AC	P27812:					
DT	01-AUG-1992 (Rel. 23, Created)					
DT	01-AUG-1992 (Rel. 23, Last sequence update)					
DT	15-DEC-1998 (Rel. 37, Last annotation update)					
DE	Natural killer cell surface protein P1-34 (NKR-P1 34).					
GN	LY55B OR LY55-B.					
OS	Mus musculus (Mouse).					
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.					
RN	NCBI_TaxID=10090;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=91349596; PubMed=1880421;					
RA	Giordana R., Trucco M.;					
RT	"Mouse NKR-P1. A family of genes selectively coexpressed in adherent					
RT	lymphokine-activated killer cells.";					
RL	J. Immunol. 147:1701-1708(1991).					
RN	[2]					
RP	SEQUENCE OF 1-29 FROM N.A.					
RX	MEDLINE=92388663; PubMed=1517565;					
RA	Giordana R., Weisberg E.P., Ip T.K., Trucco M.;					
RT	"Genomic structure and strain-specific expression of the natural					
RT	killer cell receptor NKR-P1.";					
RL	J. Immunol. 149:1957-1963(1992).					
CC	- FUNCTION: MAY FUNCTION AS SIGNAL-TRANSMITTING RECEPTOR.					
CC	- SUBCELLULAR LOCATION: Type II membrane protein.					
CC	- TISSUE SPECIFICITY: NATURAL KILLER CELLS.					
CC	- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.					
CC	-----					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration					
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CC	or send an email to license@sib-sib.ch).					
CC	-----					
CC	EMBL: M76777; AAA39823.1; -					
CC	EMBL: X64721; CAA45974.1; -					
CC	PIR: B46467; B46467.					
CC	MGI: MGI:107539; Ly55b.					
CC	InterPro: IPR001304; lectin_c.					
CC	Pfam: PF00059; lectin_c; 1.					
CC	SMART: SM00034; CLECT_1.					
CC	PROSITE: PS00615; C-TYPE_LLECTIN_1; FALSE_NEG.					
CC	PROSITE: PS50041; C-TYPE_LLECTIN_2; 1.					
CC	GLYCOPEPTIDE: Antigen; Transmembrane; Signal-anchor; Lectin.					
CC	DOMAIN 1 43					
CC	TRANSMEM 44 63					
CC	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)					
CC	(POTENTIAL).					
CC	EXTRACELLULAR (POTENTIAL).					
CC	C-TYPE LECTIN (LONG FORM).					
CC	BY SIMILARITY.					
CC	DOMAIN 64 223					
CC	DOMAIN 93 212					
CC	DISULFID 94 105					

FT DISULFID 122 210 BY SIMILARITY.
 FT DISULFID 189 202 BY SIMILARITY.
 FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 223 AA; 25157 MW; 8D04C1DEBAB9C56 CRC64;

Query Match 16.9%; Score 222.5; DB 1; Length 223;
 Best Local Similarity 32.1%; Pred. No. 4.3e-08;
 Matches 50; Conservative 22; Mismatches 77; Indels 7; Gaps 3;

QY 90 EKSFEQELQKNNQNDLQORANFSGPCPDMLMKENKY-LFHGPFGEKRNQTCOS 148
 DB 67 QKSSVQKICADVQENRHTTDCSVNLE--CPQDWLSHRDKCFRQVSVNTWEGQADCGR 124
 QY 149 LGGQLQINGADDTLFIQAIHTTSPFWIGLHRRKPGQPLWENGTPLNFOFKTRGVS 208
 DB 125 KGATLLIQDEELRFLDISEKYNFVIGLRFPLDMNWKWINGTTFNSDVKITGDT 184
 QY 209 LQYSSNCAYLQDGAFAENCILIAFSICOKKTNH 244
 B 185 -----ENGSCASISGDKVTSECSSTDNRWICQKELNH 216

RESULT 2
 NK14_MOUSE
 AC P27814;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Natural killer cell surface protein p1-40 (NKR-P1 40) (NKR-P1.9).
 GN LY55C OR LY55-C.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91349596; PubMed=1880421;
 RA Giorda R., Trucco M.;
 RT "Mouse NKR-P1. A family of genes selectively coexpressed in adherent
 RT lymphokine-activated killer cells.";
 RL J. Immunol. 147:1701-1708(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6J;
 RC MEDLINE=92373004; PubMed=1506685;
 RA Ryan J.C., Turck J., Niemi E.C., Yokoyama W.M., Seaman W.E.;
 RT "Molecular cloning of the NK1.1 antigen, a member of the NKR-P1
 RT family of natural killer cell activation molecules.";
 RL J. Immunol. 149:1631-1635(1992).
 CC -1- FUNCTION: MAY FUNCTION AS SIGNAL-TRANSMITTING RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -1- TISSUE SPECIFICITY: NATURAL KILLER CELLS.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
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 CC EMBL: M77628; AAA39824.1; -
 DR PIR: C46467; C46467.
 DR SWISS-2DPAGE: P27814; MOUSE.
 DR MGI: MGI:107538; LY55C.
 DR InterPro: IPR001304; lectin.c.
 DR Pfam: PF00059; lectin.c; 1.
 DR SMART: SM00034; CLECT; 1.

DR PROSITE: PS00615; C-TYPE LECTIN_1; FALSE_NEG.
 DR PROSITE: PS50041; C-TYPE LECTIN_2; 1.
 KW Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.
 FT DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 43 62 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT DOMAIN 63 220 (POTENTIAL).
 FT DOMAIN 90 212 EXTRACELLULAR (POTENTIAL).
 FT DISULFID 91 102 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 119 207 BY SIMILARITY.
 FT DISULFID 186 199 BY SIMILARITY.
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 220 AA; 24771 MW; 8A160B1DEDA6398F CRC64;

Query Match 16.6%; Score 218.5; DB 1; Length 220;
 Best Local Similarity 33.1%; Pred. No. 7.7e-08;
 Matches 50; Conservative 19; Mismatches 65; Indels 17; Gaps 3;

QY 95 QEELQKNNQNDLQORANFSGPCPDMLMKENKY-LFHGPFGEKRNQTCOSLGOL 153
 DB 79 QENLKTIVNLE-----CPQDWLSHRDKCFRQVSVNTWEGQADCGRKATL 126
 QY 154 LQINGADDTLFIQAIHTTSPFWIGLHRRKPGQPLWENGTPLNFOFKTRGVSLOLYS 213
 DB 127 LLIQDEELRFLDISEKYNFVIGLRFPLDMNWKWINGTTFNSDVKITGVT-----E 182
 QY 214 SSGNCAYLQDGAFAENCILIAFSICOKKTNH 244
 DB 183 NGSCASISGDKVTSECSSTDNRWICQKELNH 213

RESULT 3
 NK11_MOUSE
 AC P27811;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Natural killer cell surface protein p1-2 (NKR-P1 2) (NKR-P1.7).
 GN LY55A OR LY55.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91349596; PubMed=1880421;
 RA Giorda R., Trucco M.;
 RT "Mouse NKR-P1. A family of genes selectively coexpressed in adherent
 RT lymphokine-activated killer cells.";
 RL J. Immunol. 147:1701-1708(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92013158; PubMed=1680927;
 RA Yokoyama W.M., Ryan J.C., Hunter J.J., Smith H.R.C., Stark M.,
 RA Seaman W.E.;
 RT "CDNA cloning of mouse NKR-P1 and genetic linkage with LY-49.
 RT identification of a natural killer cell gene complex on mouse
 RT chromosome 6.";
 RL J. Immunol. 147:3229-3236(1991).
 CC -1- FUNCTION: MAY FUNCTION AS SIGNAL-TRANSMITTING RECEPTOR.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -1- TISSUE SPECIFICITY: NATURAL KILLER CELLS.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
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DR EMBL; M77676; AAA39822.1; -;
 DR EMBL; M77753; AAA39366.1; -;
 DR MGI; MGI:107540; Lys5a.
 DR InterPro; IPR001304; lectin_c.
 DR Pfam; PF00059; lectin_c.1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C-TYPE_LLECTIN_1; FALSE_NEG.
 DR PROSITE; PS50041; C-TYPE_LLECTIN_2; 1.
 DR Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.
 FT DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 43 62 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 63 227 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 93 212 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 94 105 BY SIMILARITY.
 FT DISULFID 122 210 BY SIMILARITY.
 FT DISULFID 189 202 BY SIMILARITY.
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 39 39 S -> L (IN REF. 2).
 FT SEQUENCE 227 AA; 25689 MW; 0599A2587DF0B615 CRC64;

Query Match 15.3%; Score 201.5; DB 1; Length 227;
 Best Local Similarity 32.2%; Pred. No. 1e-06;
 Matches 46; Conservative 21; Mismatches 69; Indels 7; Gaps 3;

QY 105 LOEALQGRANFSG--PCPDWLMHKNKY-LFHGFGEKKNQQTQSGGGLQINGADD 161
 DB 78 IQENINKTTDSAKLECPDWSLHDKCHVQSVNTWBEGLVDCDGKATMLTQDOPE 137
 QY 162 LTFILQAISSHSTSPWIGLHRRKPGCPWLMNGTFFLNFQFFTRGVSLQLVSSNCAYLQ 221
 DB 138 LRFLLDSIKKXNSFWFGLRATLPDMNMKMWINGSTLNSLVKLTITDPT-----ENDSCAALS 193
 QY 222 DGAVFAENCILAFSTCOCKRTNH 244
 DB 194 GDKVTFESCSNDNRWICCKEKLTH 216

RESULT 4
 FCE2_MOUSE STANDARD; PRT: 331 AA.
 AC P20693; Q61556; Q61557;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Low affinity immunoglobulin epsilon FC receptor (lymphocyte IGE
 DE receptor) (Fc-epsilon-RI) (CD23).
 GN FCE2 OR FCE2A.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RN MEDLINE=90017519; PubMed=2529542;
 RN Bettler B., Hofstetter H., Rao M., Yokoyama W.M., Kilchoff F.,
 RA Conrad D.H.;
 RT "Molecular structure and expression of the murine lymphocyte low-
 RT affinity receptor for IGE (Fc epsilon RI).";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:7566-7570(1989).
 RP SEQUENCE FROM N.A.
 RP MEDLINE=90171598; PubMed=2137845;
 RA Golnick S.O., Trounstein M.L., Yamashita L.C., Kehry M.R.,
 RA Moore K.W.;
 RT "Isolation, characterization, and expression of cDNA clones encoding

RT the mouse Fc receptor for IGE (Fc epsilon RI)1.1.";
 RL J. Immunol. 144:1974-1982(1990).
 RN [3]
 RP SEQUENCE FROM N.A. (FORMS B AND C).
 RC STRAIN=DA/2;
 RX MEDLINE=94372613; PubMed=8086828;
 RA Kondo H., Ichikawa Y., Nakamura K., Tsuchiya S.;
 RT "Cloning of cDNAs for new subtypes of murine low-affinity Fc receptor
 RT for IGE (Fc epsilon RI/CD23).";
 RL Int. Arch. Allergy Immunol. 105:38-46(1994).
 RN [4]
 RN 3D-STRUCTURE MODELING OF LECTIN DOMAIN.
 RX MEDLINE=94191542; PubMed=8142907;
 RA Padlan E.A., Helm B.A.;
 RT "Modeling of the lectin-homology domains of the human and murine low-
 RT affinity Fc epsilon receptor (Fc epsilon RI/CD23).";
 RL Receptor 3:325-341(1993).
 CC -I- FUNCTION: THIS RECEPTOR HAS ESSENTIAL ROLES IN THE REGULATION
 CC OF IGE PRODUCTION AND IN THE DIFFERENTIATION OF B-CELLS (IT IS
 CC A B-CELL-SPECIFIC ANTIGEN).
 CC -I- SUBCELLULAR LOCATION: type II membrane protein.
 CC -I- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A (SHOWN HERE), B AND C; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -I- PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).
 CC -I- MISCELLANEOUS: THERE ARE TWO KINDS OF FC RECEPTORS FOR IGE, WHICH
 CC DIFFER IN BOTH STRUCTURE AND FUNCTION: HIGH AFFINITY RECEPTORS ON
 CC BASOPHILS AND MAST CELLS AND LOW AFFINITY RECEPTORS ON LYMPHOCYTES
 CC AND MONOCYTES.
 CC -I- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC -----
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DR EMBL; M99371; AAA74898.1; -;
 DR EMBL; M34163; AAA37603.1; -;
 DR EMBL; X64223; CAA45532.1; -;
 DR EMBL; X64224; CAA45533.1; -;
 DR PIR; A43518; A43518.
 DR PDB; 1HLJ; 31-JAN-94.
 DR MGI; MGI:95497; Fce2a.
 DR InterPro; IPR001304; lectin_c.
 DR Pfam; PF00059; lectin_c.1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C-TYPE_LLECTIN_1; 1.
 DR PROSITE; PS50041; C-TYPE_LLECTIN_2; 1.
 KW IGE-binding protein; Transmembrane; Glycoprotein; Receptor; B-cell;
 KW Repeat; Lectin; Signal-anchor; Alternative splicing; 3d-structure.
 FT DOMAIN 1 23 SIGNAL-ANCHOR (POTENTIAL).
 FT TRANSMEM 24 49 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 50 331 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 185 298 C-TYPE LECTIN (LONG FORM).
 FT REPEAT 71 91
 FT REPEAT 92 112
 FT REPEAT 113 133
 FT DISULFID 183 311 BY SIMILARITY.
 FT DISULFID 183 311 BY SIMILARITY.
 FT DISULFID 186 197 BY SIMILARITY.
 FT DISULFID 214 305 BY SIMILARITY.
 FT DISULFID 282 296 BY SIMILARITY.
 FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 1 7 MEENERS -> MNSONO (IN ISOFORM B).
 FT VARSPLIC 1 7 MEENERS -> MDTHTT (IN ISOFORM C).
 FT SEQUENCE 331 AA; 37647 MW; B8C6D5F34ACDB2 CRC64;

Query Match 14.1%; Score 186; DB 1; Length 331;
 Best Local Similarity 25.4%; Pred. No. 1.5e-05;

Matches	59; Conserved	43; Mismatches	84; Indels	46; Gaps	9
QY	25	ESSQRELKIKITITRKLDKESKEDE-----	LLQMQNQEQALQRAANSSEESQREL	77	
Db	77	OSNQALAKSQVVAQSSNQQLQEQAKQMAQDSRSLSQNTLQEQEDLRNAQSQNSKISQNL	136		
QY	78	KKIDITL-----TLKLNESKESQEBELQKKNQNLQEQALQ-----	AAQFSQGPQD	122	
Db	137	NKLQDDLVNKRSLGLNTERKTATSDSL-----EKQEQEVAQKMIETLLSKQATCNH-----	CPQN	189	
QY	123	WLMHKECYLF--HGPGWEKRNQOTCSLGGQLQIQAGDLTFPIQAISSHTTSPWIGLH	181		
Db	190	WHLFQDQCYFFPKGSKMQMQLQARFACSDLOGRLVSIHSQEQDFLQMHNKIKDS--	WIGLQ	247	
QY	182	RKKPGQPMWEMNGTPLNQFFKTRGVSLQLYSSNCAYLQDQGVAFENQILI	233		
Db	248	DLIMEGEFVMSQSPVG-----YSNMNDFERNNGQ--GEDCYVM	285		

	RESULT	5		
NK13_RAT			STANDARD:	PRT: 223 AA.
D	NK13_RAT			
CC	p27471.			
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DT	01-JUN-1994 (Rel. 29, Last annotation update)			
DE	Natural killer cell surface protein P1-3.2.3 (NKR-P1 3.2.3) (Antigen 3.2.3).			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90378305; PubMed=2399464;			
RA	Glorida R., Rudert W.A., Vavassori C., Chambers W.H.,			
RA	Hiserodt J.C., Trucco M.;			
RL	"NKR-P1, a signal transduction molecule on natural killer cells.";			
RL	Science 249:1298-1300(1990).			
CC	-1 FUNCTION: MEDIATES TRANSMEMBRANE SIGNALING IN NATURAL KILLER			
CC	(NK) CELLS AND SO MAY ACT AS A RECEPTOR ABLE TO SELECTIVELY			
CC	TRIGGER NK CELL ACTIVITY.			
CC	-1 SUBUNIT: HOMODIMER.			
CC	-1 SUBCELLULAR LOCATION: Type II membrane protein.			
CC	-1 TISSUE SPECIFICITY: NATURAL KILLER CELLS.			
CC	-1 MISCELLANEOUS: LIGAND BINDING MAY BE CALCIUM DEPENDENT.			
CC	-1 SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ ,			
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CC	-----			
DR	EMBL, M62891, AAA41710.1; -.			
DR	PIR, A35917; A35917.			
DR	InterPro, IPR001304; lectin_c.			
DR	Pfam, PF00059; lectin_c: 1.			
DR	SMART, SM00034; CLCCT: 1.			
DR	PROSITE, PS00615; C-TYPE_LLECTIN_1; FALSE_NEG.			
DR	PROSITE, PS50041; C-TYPE_LLECTIN_2; 1.			
RW	Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.			
FT	DOMAIN 1 43			
FT	CYTOPLASMIC (POTENTIAL).			
FT	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)			
FT	TRANSMEM 44 63			
FT	(POTENTIAL).			
FT	EXTRACELLULAR (POTENTIAL).			
FT	DOMAIN 64 223			
FT	DOMAIN 93 212			
FT	DISULFID 94 105			
FT	DISULFID 122 210			
FT	BY SIMILARITY.			
FT	DISULFID 189 202			
FT	BY SIMILARITY.			
FT	CARBOHYD 82 82			
FT	N-LINKED (GLCNAC...) (POTENTIAL).			

	CAROHVD	143	143	N-LINKED (GLC/MNC . . .) (POTENTIAL).
FT	CAROHVD	169	169	N-LINKED (GLC/MNC . . .) (POTENTIAL).
SQ	SEQUENCE	223 AA;	245S1 MW;	FCD12B212DDF4330 CRC64,
	Query Match	13.2%;	Score 174;	DB 1; Length 223;
	Best Local Similarity	27.3%;	Pred. NO. 6e-05;	
	Matches	38; Conservative	26; Mismatches	69; Indels 6; Gaps 3.
OY	105 LOEALORANESG-PQPDWLHKENCY-LFHGPGEWKKRQTCOSLGQLIQINGADDL	162		
	: : : : : : : : : : : : : : : :			
Db	79 IOENSKTSPKLCIKPKMDLSHRCKCFHVSQTSTJTWKSLADCGSGKATLLVDOEEI	138		
	: : : : : : : : : : : : : : : :			
OY	163 TFLDAISHTTSPPFMICGHRRKRGQPWMLENCTPINFQEFKTRGVSLQAYSSNCAVLQD	222		
	: : : : : : : : : : : : : : : :			
Db	139 RFLRNUTKRISSEFWGLSYTLSDENKMKNINSTLNSDVLSITGT---EKDSQASVQ	194		
	: : : : : : : : : : : : : : : :			
OY	223 GAVFAENCILIAFSICQKK	241		
	: : : : : : : : : : : : : : : :			
Db	195 DKVLESQCDSQNIWVCQKE	213		

CD94_HUMAN	STANDARD:	PRT:	179 AA.
DR	01-NOV-1997 (Rel. 35, Created)		
DR	01-NOV-1997 (Rel. 35, Last sequence update)		
DR	15-DEC-1998 (Rel. 37, Last annotation update)		
DE	Natural killer cells antigen CD94 (KR43) (Killer cell lectin-like receptor subfamily D, member 1).		
GN	KLKRD1 OR CD94.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Blood;		
RX	MEDLINE=96011848; PubMed=7589107;		
RA	Chang C., Rodriguez A., Carretero M., Lopez-Botet M., Phillips J.H.,		
RA	Lanier L.L.;		
RT	"Molecular characterization of human CD94: a type II membrane		
RT	glycoprotein related to the C-type lectin superfamily.";		
RL	Eur. J. Immunol. 25:2433-2437(1995).		
CC	- FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHC		
CC	CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.		
CC	- SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH NKG2 FAMILY		
CC	MEMBERS.		
CC	- I- SUBCELLULAR LOCATION: Type II membrane protein.		
CC	- I- TISSUE SPECIFICITY: NATURAL KILLER CELLS.		
CC	- I- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.		
CC	- I- DATABASE: NAME=PROW; NOTE=CD guide CD94 entry;		
CC	WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd94.htm".		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
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CC	-----		
DR	EMBL: U30610; AAC50291.1; -.		
DR	MIM: 602894; -.		
DR	InterPro: IPR001304; lectin_c.		
DR	SMART: PF000039; lectin_c.1.		
DR	SMART: SM000034; CLECT; 1.		
DR	PROSITE: PS00615; C-TYPE LECTIN_1; FALSE_NEG.		
DR	PROSITE: PS00041; C-TYPE LECTIN_2; 1.		
KW	Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin.		
FT	DOMAIN 1 10		
FT	TRANSMEM 11 31		
FT	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)		

FT	DOMAIN	32	179	(POTENTIAL).
FT	DOMAIN	98	176	EXTRACELLULAR (POTENTIAL).
FT	DISULFID	61	72	C-TYPE LECTIN (LONG FORM).
FT	DISULFID	89	174	BY SIMILARITY.
FT	DISULFID	152	166	BY SIMILARITY.
FT	CARBOHYD	83	83	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	132	132	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	179 AA;	20497 MW;	1864D99EBD9583A/ CRC64;
Query Match		12.6%;	Score 166;	DB 1; Length 179;
Best Local Similarity		31.6%;	Pred. No. 0.00016;	
Matches	36;	Conservative	20;	Mismatches 48; Indels 10; Gaps
Qy	119	CPQDMLMKKNCYLFHG-PFGWEKRRQTCQSLAGGQLDQINGADDLFTLLQAISSHTTSPW	177	
Db	61	COEKWVGRCNCYFLSSBQKTWNESEHLCASQSSLLDLDQNDDELDF--MSSSQOFYW	116	
Qy	178	IGLHRRKGGQWPLWNGTPLNFOFKTRGVSLDLTSSSNC-AYLDDGAFAENC	230	
Db	117	IGLSSEHTTAMWNGSALSQYLF-----SEFTTNTKNCIAYNNGNALDESC	166	
RESULT	7			
FCE2_HUMAN				
ID	FCE2_HUMAN	STANDARD;	PRT;	321 AA.
AC	P06734;			
DT	01-JAN-1988	(Rel. 06, Created)		
DT	01-JAN-1988	(Rel. 06, Last sequence update)		
DT	16-OCT-2001	(Rel. 40, Last annotation update)		
DE	Low affinity immunoglobulin epsilon FC receptor (Lymphocyte Ige			
DE	receptor) (Fc-epsilon-RI) (CD23) (BLAST-2) (Immunoglobulin E-binding			
DE	factor).			
GN	FCER2 OR IGEBF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87118255; PubMed=2949326;			
RA	Ikuta K., Takami M., Kim C.W., Honjo T., Miyoshi T., Tagaya Y.,			
RA	Kawabe T., Yodoi J.;			
RT	"Human lymphocyte Fc receptor for Ige: sequence homology of its			
RT	cloned cDNA with animal lectins.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 84:819-823(1987).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87051737; PubMed=2877743;			
RA	Kikuchi H., Inui S., Sato R., Barsumian E.L., Owaki H.,			
RA	Yamasaki K., Kaisho T., Uchibayashi N., Hardy R.R., Hirano T.,			
RA	Tsunasawa S., Sakiyama F., Suenura M., Kishimoto T.;			
RT	"Molecular structure of human lymphocyte receptor for immunoglobulin			
RT	E.";			
RL	Cell 47:657-665(1986).			
RL	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87218454; PubMed=3034567;			
RA	Luedin C., Horstetter H., Sarfelt M., Levy C.A., Suter U., Alaino D.,			
RA	Kilchherr E., Frost H., Deslepesse G.;			
RT	"Cloning and expression of the cDNA coding for a human lymphocyte Ige			
RT	receptor.";			
RL	Embo J. 6:109-114(1987).			
RL	[4]			
RP	PARTIAL SEQUENCE, AND DISULFIDE BONDS.			
RX	MEDLINE=93038513; PubMed=1417742;			
RA	Rose K., Turcattl G., Graber P., Pochon S., Regamey P.-O.,			
RA	Jansen K.U., Magnenet E., Auboney N., Bonnefoy J.-Y.;			
RT	"Partial characterization of natural and recombinant human soluble			
RT	CD23.";			
RL	Biochem. J. 286:819-824(1992).			
RL	[5]			

RP	ALTERNATIVE SPLICING.
RX	MEDLINE=69028672; PubMed=2972386;
RA	Yokota A., Kikucani H., Tanaka T., Sato R., Barsmian E.L.,
RA	Suemura M., Kishimoto T.;
RT	"Two species of human Fc epsilon receptor II (Fc epsilon RI/CD23):
RT	tissue-specific and IL-4-specific regulation of gene expression.";
RL	Cell 55:611-618(1988).
RN	[6]
RP	3D-STRUCTURE MODELING OF LECTIN DOMAIN.
RX	MEDLINE=94191542; PubMed=8142907;
RA	Padian E.A., Helm B.A.;
RT	"Modeling of the lectin-homology domains of the human and murine low-
RT	affinity Fc epsilon receptor (Fc epsilon RI/CD23).";
RL	Receptor 3:325-341(1993).
RN	[7]
RP	3D-STRUCTURE MODELING OF 173-285.
RX	MEDLINE=96276216; PubMed=8745401;
RA	Bajorath J., Aruffo A.;
RT	"Structure-based modeling of the ligand binding domain of the human
RT	cell surface receptor CD23 and comparison of two independently
RT	derived molecular models.";
RL	Protein Sci. 5:240-247(1996).
CC	-I- FUNCTION: THIS RECEPTOR HAS ESSENTIAL ROLES IN THE REGULATION
CC	OF ICE PRODUCTION AND IN THE DIFFERENTIATION OF B-CELLS (IT IS
CC	A B-CELL-SPECIFIC ANTIGEN).
CC	-I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS
CC	A SOLUBLE EXCRETED FORM.
CC	-I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE
CC	PRODUCED BY ALTERNATIVE SPLICING.
CC	-I- PTM: N- AND O-GLYCOSYLATED.
CC	-I- MISCELLANEOUS: THERE ARE TWO KINDS OF FC RECEPTORS FOR ICE, WHICH
CC	DIFFER IN BOTH STRUCTURE AND FUNCTION: HIGH AFFINITY RECEPTORS ON
CC	BASOPHILS AND MAST CELLS AND LOW AFFINITY RECEPTORS ON LYMPHOCYTES
CC	AND MONOCYTES.
CC	-I- SIMILARITY: CONTRAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC	-I- DATABASE: NAME-PROW; NOTE-CD guide CD23 entry.
CC	WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd23.htm".
CC	-----
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; M15059; AAA52434.1; ;
DR	EMBL; M14766; AAA52435.1; ;
DR	EMBL; X04772; CAA28465.1; ;
DR	EMBL; M23562; AAA52433.1; ;
DR	PIR; A26067; LNHER.
DR	PIR; A26164; A26164.
DR	PIR; A26589; A26589.
DR	PIR; A31924; A31924.
DR	PIR; JL0132; JL0132.
DR	PDB; 1HLJ; 3J-JAN-94.
DR	PDB; 1KJE; 03-APR-96.
DR	MIM; I51445; .
DR	InterPro; IPRO01304; lectin_c.
DR	SMART; PF00059; lectin_c; 1.
DR	SMART; SM00034; CLECT; 1.
DR	PROSITE; PS00615; C_Type_Lectin_1; 1.
DR	PROSITE; PS50041; C_Type_Lectin_2; 1.
KW	IgE-binding protein; Transmembrane; Glycoprotein; Receptor; B-cell;
KW	Repeat; Lectin; Signal-anchor; Alternative splicing; 3D-structure.
FT	CHAIN 1 321
FT	DOMAIN 150 321
FT	TRANSMEM 22 47
FT	DOMAIN 48 321
FT	DOMAIN 162 284
FT	SITE 149 150
FT	CLEAVAGE.
FT	(POTENTIAL).
FT	(POTENTIAL).
FT	(LONG FORM).
FT	(C-TYPE LECTIN (LONG FORM)).
FT	(TYPE-II MEMBRANE PROTEIN)
FT	(CYTOPLASMIC (POTENTIAL)).
FT	(SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN))
FT	(EXTRACELLULAR (POTENTIAL)).
FT	(C-TYPE LECTIN (LONG FORM)).
FT	CLEAVAGE.

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FT REPEAT 69 89
FT REPEAT 90 110
FT REPEAT 111 131
FT DISULFID 160 288 BY SIMILARITY.
FT DISULFID 163 174 BY SIMILARITY.
FT DISULFID 191 282
FT DISULFID 255 273
FT CARBOHYD 63 63
FT CARBOHYD 1 7
FT VARSPLIC 269 269 N-MEGLYS -> NMPISO (IN ISOFORM B).
FT CONFLICT 1 269 N -> T (IN REF. 3).
SQ SEQUENCE 321 AA; 36468 MW; F86708C0E6515887 CRC64;

Query Match 12.5%; Score 165.5; DB 1; Length 321;
Best Local Similarity 28.7%; Pred. No. 0.00032;
Matches 51; Conservative 33; Mismatches 75; Indels 19; Gaps 7;

QY 28 QRLKRGKIDITRKDEKSEKQEL-----LQMIQNLQALQORANSESEKQELKIDT 83
DB 78 QMOKSOSTQISQELERAEQRLKSQDELQSWNL-NGIQ-ADLSSEKQELNER-- 131
QY 84 LTLKNEKSEKQELQKQNLQALQORANF-SGPCPQDMLMKKCYLF-HGPFQMEK 141
DB 132 -----NEASDLERLREYVTKLMELOVSSGFCNCTPEKWINFQKCYLFQKGTQKQVH 186
QY 142 NRQTCOSLGGQLQINGADDLFTILOAISHTSPFWIGLHRRKPGQPMLENGTPI 199
DB 187 ARYACDMEQOLVSIHSPEDQFLTKHSHSGS--WIGLNLDLKGFQIWDGSHVDY 242

RESULT 8
LECT_HUMAN STANDARD; PRT; 311 AA.
ID LECT_HUMAN
AC P07307;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Asialoglycoprotein receptor 2 (Hepatic lectin H2) (ASGP-R) (ASGPR).
GN ASGR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86016723; PubMed=3863106;
RA Spies M., Lodish H.F.;
RT "Sequence of a second human asialoglycoprotein receptor: conservation of two receptor genes during evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 82:6465-6469(1985).
CC -1- FUNCTION: MEDIATES THE ENDOCYTOSIS OF PLASMA GLYCOPROTEINS TO WHICH THE TERMINAL SIALIC ACID RESIDUE ON THEIR COMPLEX CARBOHYDRATE MOIETIES HAS BEEN REMOVED. THE RECEPTOR RECOGNIZES TERMINAL GALACTOSE AND N-ACETYLGLUCOSAMINE UNITS. AFTER LIGAND BINDING TO THE RECEPTOR, THE RESULTING COMPLEX IS INTERNALIZED AND TRANSPORTED TO A SORTING ORGANELLE, WHERE RECEPTOR AND LIGAND ARE DISSOCIATED. THE RECEPTOR THEN RETURNS TO THE CELL MEMBRANE SURFACE.
CC -1- SUBUNIT: THE FUNCTIONING LIGAND-BINDING UNIT OF THIS RECEPTOR IS THOUGHT TO BE AT LEAST A DIMER.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN HEPATIC PARENCHYMAL CELLS.
CC -1- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
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CC -----
DR EMBL: M11025; AAB59519.1; -.
DR PIR: A25179; LNHU2A.
DR HSSP: P06734; 1KJE.
DR MIM: 108361; -.
DR InterPro: IPR001304; lectin_C.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
KW Lectin; Glycoprotein; Receptor; Endocytosis; Transmembrane;
KW Calcium; Signal-anchor; Phosphorylation.
FT DOMAIN 1 58 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 59 79 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT DOMAIN 80 311 (POTENTIAL).
FT SITE 176 302 EXTRACELLULAR (POTENTIAL).
FT DISULFID 5 8 C-TYPE LECTIN (LONG FORM).
FT DISULFID 177 188 ENDOCYTOSIS SIGNAL (POTENTIAL).
FT DISULFID 205 300 BY SIMILARITY.
FT DISULFID 278 292 BY SIMILARITY.
FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .).
FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .).
FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .).
FT MOD_RES 12 12 PHOSPHORYLATION.
SQ SEQUENCE 311 AA; 35191 MW; 82C78FEC8FBA316 CRC64;

Query Match 12.5%; Score 164.5; DB 1; Length 311;
Best Local Similarity 25.1%; Pred. No. 0.00036;
Matches 59; Conservative 36; Mismatches 81; Indels 59; Gaps 11;

QY 51 ELQMIQNLQALQORANSS-----ESSQRLKRGKIDITLT 85
DB 88 QLOAELSLKLEAFNFSSTLEVOAISTHGSVGDKITSLGAKLEKQOQDLKADHDALL 147
QY 86 LKLNKESKE-----QELLQKQNLQALQORANFSGPCPQDMLMKKCYLF-HGPFQ 138
DB 148 FHLKHPVDLRFVACQMLHLSNGS-----QRTC-----CPVNVVEHQSGCYWFSHGKA 197
QY 139 WEKNRQTCOSLGGQLQINGADDLFTILOAISHTSPF--WIGLHRRKPGQPMLENGTPI 196
DB 198 WAEAEKTCOLENAHLVYINSNEQKFTVQ-----HTNFPNWIGL--TDSGSKWNVGCTD 251
QY 197 LNFQFEKTRGVSL-----QLYSSSNCAVYL-DGAVFAENCILIAFSICQKTN 243
DB 252 YRHN-YKNMVAVTQDNNHGHGELGSEDCVEYQPDGRWNNDDPCLQVYRWVCEKRRN 305

RESULT 9
KUCR_RAT STANDARD; PRT; 550 AA.
ID KUCR_RAT
AC P10716;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kupfer cell receptor.
DE KCLR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 83-104.
RX MEDLINE=88227939; PubMed=2836387;
RA Hoyle G.W., Hill R.L.;
RT "Molecular cloning and sequencing of a cDNA for a carbohydrate binding receptor unique to rat Kupfer cells."
RL J. Biol. Chem. 263:7487-7492(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91107689; PubMed=1846367;
RA Hoyle G.W., Hill R.L.;

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RT      "Structure of the gene for a carbohydrate-binding receptor unique to
RT      rat Kupffer cells."
CC      J. Biol. Chem. 266:1850-1857(1991).
CC      -!- FUNCTION: RECEPTOR WITH AN AFFINITY FOR GALACTOSE AND FUCOSE.
CC      -!- COULD BE INVOLVED IN ENDOCYTOSIS.
CC      -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC      -!- TISSUE SPECIFICITY: KUPFFER CELLS.
CC      -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL: J03734; AAA4172.1; -
DR      EMBL: M55532; AAA40892.1; -
DR      PIR: A28166; A28166.
DR      PIR: A38674; A38674.
DR      HSSP: P20693; 1HLJ.
DR      InterPro: IPR000017; Syntaxin.
DR      InterPro: IPR001304; lectin_c.
DR      Pfam: PF00059; lectin_c; 1.
DR      SMART: SM00034; CLECT; 1.
DR      SMART: SM00503; SYN; 1.
DR      PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
DR      PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
DR      Receptor; Transmembrane; Glycoprotein; Lectin; Signal-anchor;
DR      Endocytosis.
RT      DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).
RT      TRANSMEM 43 69 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
RT      (POTENTIAL).
RT      DOMAIN 70 550 EXTRACELLULAR (POTENTIAL).
RT      DOMAIN 438 538 C-TYPE LECTIN (SHORT FORM).
RT      DISULFID 440 536 BY SIMILARITY.
RT      DISULFID 516 528 BY SIMILARITY.
RT      CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
RT      CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
RT      CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
RT      CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
RT      CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).
RT      CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).
RT      SEQUENCE 550 AA; 61104 MW; 9358ACF4C306270 CRC64;

Query Match 12.4%; Score 163.5; DB 1; Length 550;
Best Local Similarity 22.8%; Pred. No. 0.00076;
Matches 62; Conservative 55; Mismatches 112; Indels 43; Gaps 12;

OY      2 TFDKMKRPN--DEPDQKSGCKRKRKRESEQRELKGIKIDITITKLDKSKSEDELLQMIQN 58
DB      283 TLTAIOYANAGHLEOTDTIOGLKAKQVLSSTSLNSQIEYVNGKLSQDSLEOTLRDLSLD 342
OY      59 LQALQARANSSEESQRELKGIKIDITITKLNKSKSEDELLQKONLQALOR--AANFS 116
DB      343 V-SALKSNVQMLQSNLQAKAAYVSLKTLGL-EATKTLAKIQQGQSDLEALQAAVAHTQ 400
OY      117 GP-----CPQDMLHKKENCYLF-HGPFGEKNRROTCSLGGQQLQINGADITFTL 166
DB      401 GQKTONVQLQIMQDMKFKNGKFFYSRDKSWHAEANECVSGAHLASVTSQEQEAFV 460
OY      167 Q---AISHTTSPFVIGLRKKRPGPWLWNGTFLNFOPEKTKGVSLOLYSSNCAYLQDG 223
DB      461 QITNAVH-----WIGLIDQGTGEGMKRWYDGTG--FDYQSR-----REWRKGPDPNWRHG 509
OY      224 AVFAENCIL-----AFS-ICQKKTN 243
DB      510 NGEREDCVHLQRMWMDMACGTAYNWCKKSTD 541

RESULT 10

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NKG2C_HUMAN
ID      NKG2C_HUMAN STANDARD: PRT; 231 AA.
AC      P26717; 043802;
DT      01-AUG-1992 (rel. 23, Created)
DT      01-MAR-2002 (rel. 41, Last sequence update)
DT      01-MAR-2002 (rel. 41, Last annotation update)
DE      NKG2-C type II integral membrane protein (NKG2-C activating NK
DE      receptor).
GN      KLRG2 OR NKG2C.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1-]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=91178434; PubMed=2007850;
RA      Houchins J.P., Yabe T., McSherry C., Bach F.H.;
RT      "DNA sequence analysis of NKG2, a family of related cDNA clones
RT      encoding type II integral membrane proteins on human natural killer
RT      cells."
RL      J. Exp. Med. 173:1017-1020(1991).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98350122; PubMed=9683661;
RA      Glienke J., Sobanov Y., Brostjan C., Steffens C., Nguyen C.,
RA      Lehrach H., Hofer E., Francis F.;
RT      "The genomic organization of NKG2C, E, F, and D receptor genes in the
RT      human natural killer gene complex."
RL      Immunogenetics 48:165-173(1998).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      Tissue=Lymphoid;
RL      Biocompare R.;
RT      Submitted (May-1997) to the EMBL/Genbank/DBJ databases.
CC      -!- FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHC
CC      CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.
CC      -!- SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH CD94.
CC      -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC      -!- TISSUE SPECIFICITY: NATURAL KILLER CELLS.
CC      -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC      -----
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CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL: X54869; CA38651.1; -
DR      EMBL: AJ001684; CA04922.1; -
DR      EMBL: Y13055; CA73498.1; -
DR      PIR: PTO374; PTO374.
DR      MIM: 602891;
DR      InterPro: IPR001304; lectin_c.
DR      Pfam: PF00059; lectin_c; 1.
DR      SMART: SM00034; CLECT; 1.
DR      PROSITE: PS00615; C-TYPE_LECTIN_1; FALSE_NEG.
DR      PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
KW      Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
KW      Glycoprotein.
RT      DOMAIN 1 70 CYTOPLASMIC (POTENTIAL).
RT      TRANSMEM 71 93 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
RT      (POTENTIAL).
RT      DOMAIN 94 231 EXTRACELLULAR (POTENTIAL).
RT      DOMAIN 116 229 C-TYPE LECTIN (LONG FORM).
RT      DISULFID 117 128 BY SIMILARITY.
RT      DISULFID 145 227 BY SIMILARITY.
RT      DISULFID 206 219 BY SIMILARITY.
RT      CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
RT      CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
RT      CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
RT      CONFLICT 161 161 M -> I (IN REF. 1).

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SQ SEQUENCE 231 AA; 26072 MW; 6B971EECDJ542930 CRC64;
 Query Match 12.3%; Score 162.5; DB 1; Length 211;
 Best Local Similarity 23.0%; Pred. No. 0.00035;
 Matches 53; Conservative 37; Mismatches 101; Indels 39; Gaps 7;
 QY 18 SCGRKPKESQRELKGIIDITRKLDKSKQEBELLQMIQLOEA-----LQR 65
 Db 12 SLADDPKRO-QRKPKKSSSI-----SGTEGEIFQVELNLQNPISLHOCIDKIDYDQG 63
 QY 66 AANSSESOEELKGIIDITRKLDKSKQEBELLQMIQLOEAORANSGPQPMW 125
 Db 64 LRPPEKLEAEVGLIICIVLMAVLTIVLIPLEONNSPNTQKARHCNCPPEMIT 123
 QY 126 HKENCYLFHGPFG-----WEKNROTCOSLGOLQINGADDPITLQASHITSPFWIGL 180
 Db 124 YSNICY-----IGKERTWESLACTSKNSLSLSTINEEMKFLASILPSS-----WIGV 175
 QY 181 HRRKPGQPMLENGTPIINFQFETRGVSIQLYSSNCAYLQDGAFAENC 230
 b 176 FRSSHHPTWITINGLAFKHKIKSDNAEL-----NCAYLVNRLKSAOC 219
 RESULT 11
 KUCR_MOUSE STANDARD; PRT; 548 AA.
 ID KUCR_MOUSE
 AC F70194;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kupfer cell receptor.
 GN KCLR.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RA STRAIN-BALB/C; TISSUE-Liver;
 RA Takekawa R., Magatsuna H., Nomoto C., Watanabe Y., Akaike T.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR WITH AN AFFINITY FOR GALACTOSE AND FUCOSE.
 CC -1- COULD BE INVOLVED IN ENDOCYTOSIS.
 CC -1- SUBCELLULAR LOCATION: TYPE II membrane protein.
 CC -1- TISSUE SPECIFICITY: KUPFER CELLS.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL: D88577; BAA13647.1; -.
 DR HSSP: P20693; IHLJ.
 DR MGD: MGI:1859834; KcLr.
 DR InterPro: IPR001304; lectin_c.
 DR Pfam: PR00059; lectin_c; 1.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PS00615; C-TYPE_LLECTIN_1; 1.
 DR PROSITE: PS50041; C-TYPE_LLECTIN_2; 1.
 KM Receptor; Transmembrane; Glycoprotein; Lectin; Signal-anchor;
 Endocytosis.
 FT DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 43 69 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT DOMAIN 70 548 EXTRACELLULAR (POTENTIAL).
 FT DISULFID 438 538 C-TYPE LECTIN (SHORT FORM).
 FT DISULFID 440 536 BY SIMILARITY.
 FT DISULFID 516 528 BY SIMILARITY.

FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 548 AA; 61268 MW; 6F645E820E73BD9 CRC64;
 Query Match 12.2%; Score 160.5; DB 1; Length 548;
 Best Local Similarity 25.5%; Pred. No. 0.0012;
 Matches 56; Conservative 36; Mismatches 93; Indels 35; Gaps 9;
 QY 2 TFDKMKRPN---DEPDQSCGRKPKESQRELKGIIDITRKLDKSKQEBELLQMIQLOEA 54
 Db 283 TLTAQTQKANGHLQPTDAQIGLAKELKSTSLMSRIEYVNGQKDAARELQTLRLDLS 342
 QY 55 -----MIQNLQEAORANSGPQPMWLMHKENCYLF-HGPFGEKRNROTCOSLGOLQING 99
 Db 343 VSALKSNVOMLQSNLQAKTEMOTLKADLA-TRALAKIQEGONRLGALQEAFAAQOE 401
 QY 100 QKNQNLQEAORANSGPQPMWLMHKENCYLF-HGPFGEKRNROTCOSLGOLQING 158
 Db 402 OKTON--QVLDLIA-----QNMKTFNGNFTYRSRDKKPKREKCTSGAHLASYTS 452
 QY 159 ADLFTLQALISHTSPFWIGLARRKPKQPMWLENGTPI 198
 Db 453 QEQAFVLYQTS--SGDHWIGLTDQGTGIGRWVDGTPEN 490
 RESULT 12
 NKGE_HUMAN STANDARD; PRT; 240 AA.
 ID NKGE_HUMAN
 AC 007444;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE NKG2-E type II integral membrane protein (NKG2-D activating NK
 receptor).
 GN KLRG3 OR NKG2E.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC SEQUENCE FROM N.A.
 RA MEDLINE=94102823; Pubmed=8276468;
 RA Adamkiewicz T.V., McSherry C., Bach F.H., Houchins J.P.;
 RT "Natural killer lectin-like receptors have divergent carboxy-terminal,
 RT distinct from C-type lectins.";
 RL Immunogenetics 39:218-218(1994).
 RN [2]
 RC SEQUENCE FROM N.A.
 RX MEDLINE=98350122; Pubmed=9683661;
 RA Glieneck J., Sobanov Y., Brostjan C., Steffens C., Nguyen C.,
 RA Lehrach H., Hoyer E., Francis F.;
 RT "The genomic organization of NKG2C, E, F, and D receptor genes in the
 RT human natural killer gene complex.";
 RL Immunogenetics 48:163-173(1998).
 CC -1- FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHC
 CC CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.
 CC -1- SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH CD94.
 CC -1- TISSUE SPECIFICITY: NATURAL KILLER CELLS.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
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CC -----
DR EMBL; L14542; AAA16833.1;
DR EMBL; AJ001685; CAA04923.1;
DR MIM; 602892;
DR InterPro; IPR001304; lectin_c.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.
DR Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
KW Glycoprotein.
FT DOMAIN 1 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 93 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT DOMAIN 94 240 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 116 230 C-TYPE LECTIN (LONG FORM).
FT DISULFID 117 128 BY SIMILARITY.
FT DISULFID 207 220 BY SIMILARITY.
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 240 AA; 27012 MW; 20691FB2127AD8A6 CRC64;

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Query Match 12.1%; Score 159; DB 1; Length 240;
Best Local Similarity 22.9%; Pred. No. 0.00061;
Matches 53; Conservative 40; Mismatches 98; Indels 40; Gaps 8;

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QY 18 SCGKKPKESQRELKGIIDITRKLEKSEKEDELLQNIQOE-----LOR 65
DB 12 SLADDPKPO-QRKPKGNKSSI-----SGTEQEIFQVELNQNLSLNHOGIDKIYDCG 63
QY 66 AANSESEQRELKGIIDITRKLEKSEKEDELLQNIQOEALQRAANFSGPCPDMLM 125
DB 64 LLPEKLTAEVLGITCIYLAIVATYLVLPFLQNNSPTRKQKAPCHCEBEWTT 123
QY 126 HKENCYLFGHPG-----WEKNRQTCQL-GGQLQINGADDLPLIQAISHTSPFWIG 179
DB 124 YNSNGY----IGKERRWEESLQACASKNSSLSIDNEEMKTLASLPSS-----WIG 175
QY 180 LHRKKPGPWLMENGTPLNFOFETKRGVSLQIYSSNCAYLQDGAFAENC 230
DB 176 VFRNSHHWPVTINGLAFKHE-----IKSDHARNCAMLHVRLISDQC 220

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RESULT 13
ID NKGD_HUMAN STANDARD; PRT; 216 AA.
AC P26718;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE NKG2-D type II integral membrane protein (NKG2-D activating NK
DE receptor).
GN KLRK4 OR NKG2D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91178434; PubMed=2007850;
RA Houchns J.P., Yabe T., McSherry C., Bach F.H.;
RT "DNA sequence analysis of NKG2, a family of related cDNA clones
RT encoding type II integral membrane proteins on human natural killer
RT cells.";
RL J. Exp. Med. 173:1017-1020(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98350122; PubMed=9683661;
RA Gliente J., Sobanov Y., Brostjan C., Steffens C., Nguyen C.,
RA Leinach H., Hoyer E., Francis F.;
RT "The genomic organization of NKG2C, E, F, and D receptor genes in the

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RT human natural killer gene complex.";
RL Immunogenetics 48:163-173(1998).
CC -!- FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHC
CC CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.
CC -!- SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH CD94.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- TISSUE SPECIFICITY: NATURAL KILLER CELLS.
CC -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -----
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CC -----

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DR EMBL; X54870; CAA38652.1;
DR EMBL; AJ001687; CAA04925.1;
DR EMBL; AJ001688; CAA04925.1; JOINED.
DR EMBL; AJ001689; CAA04925.1; JOINED.
DR PIR; P03375; P03375.
DR PIR; S19110; S19110.
DR MIM; 602893;
DR InterPro; IPR001304; lectin_c.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.
DR Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
KW Glycoprotein.
FT DOMAIN 1 51 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 52 72 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT FT (POTENTIAL).
FT DOMAIN 73 216 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 98 213 C-TYPE LECTIN (LONG FORM).
FT DISULFID 99 110 BY SIMILARITY.
FT DISULFID 127 211 BY SIMILARITY.
FT DISULFID 189 203 BY SIMILARITY.
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 216 AA; 25274 MW; C22F6BD533D7800E CRC64;

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Query Match 12.0%; Score 158.5; DB 1; Length 216;
Best Local Similarity 27.6%; Pred. No. 0.00059;
Matches 40; Conservative 26; Mismatches 62; Indels 17; Gaps 5;

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QY 102 NONLOEALORANFSGPCPDMLMHKENCY-LFHGPFGEKRNQTCQSLGGQLQINGAD 160
DB 84 NOEVOIPL--TSTYCGPCFKNNICYNKCTOFFDESKNMYESQASCSQNASLKYSE 141
QY 161 DLFTLIQAISHTSPFWIGLARRKPGQPLWENGTPLN---PQFETKRGVSLQIYSSNC 217
DB 142 DODLLKLVKSY----HMMGLVHIPTNGSQWEDGSLTSLNLLTIEMQGDCAVLASSPK 197
QY 218 ATLQDGAFAVENCILIASISOCKKT 242
DB 198 GYI-----ENCSTPNYICMORT 215

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RESULT 14
ID KLR5_MOUSE STANDARD; PRT; 266 AA.
AC Q60652;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Killer cell lectin-like receptor 5 (T-cell surface glycoprotein
DE LY-49E) (LY49-E antigen).
GN KLR5 OR LY49E OR LY-49E OR LY49-E.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Spleen;
RX MEDLINE=94300068; PubMed=8027540;
RA Smith H.R.C., Karlhofer F.M., Yokoyama W.M.;
RT "Ly-49 multigene family expressed by IL-2-activated NK cells.";
RL J. Immunol. 153:1068-1079(1994).
CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR CLASS I MHC.
CC -1- SUBUNIT: HOMODIMER. DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
DR EMBL: U10091; AAA50219.1;
DR MGI: 101903; K1ra5.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; Lectin_c_1.
DR SMART: SM00034; CLECT_1.
DR PROSITE: PS00615; C-TYPE LECTIN_1; FALSE_NEG.
DR PROSITE: PS50041; C-TYPE LECTIN_2; 1.
KW T-cell; Glycoprotein; Antigen; Transmembrane; Cell adhesion;
KW Signal-anchor; Lectin; Receptor; Multigene family.
FT DOMAIN 1 44 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 45 66 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT 67 266 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 143 261 C-TYPE LECTIN (LONG FORM).
FT DISULFID 171 257 BY SIMILARITY.
FT DISULFID 236 249 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 266 AA; 30843 MW; B8B07F221875049C CRC64;

Query Match 11.8%; Score 156; DB 1; Length 266;
Best Local Similarity 27.6%; Pred. No. 0.0011;
Matches 54; Conservative 30; Mismatches 96; Indels 16; Gaps 8;

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DE Early activation antigen CD69 (Early T-cell activation antigen p60)
DE (GP32/28) (Leu-23) (MUR-3) (EAI) (BL-AC/P26) (Activation Inducer
DE molecule) (AIM).
GN CD69.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=93340630; PubMed=8496594;
RA Hamann J., Fiebig H., Strauss M.;
RT "Expression cloning of the early activation antigen CD69, a type II
RT integral membrane protein with a C-type lectin domain.";
RL J. Immunol. 150:4920-4927(1993).
RN [2]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 96-103; 128-146 AND 189-199.
RC TISSUE=Blood;
RX MEDLINE=93340630; PubMed=8340758;
RA Lopez-Cabrera M., Santis A.G., Fernandez-Ruiz E., Blacher R.,
RA Esch F., Sanchez-Mateos P., Sanchez-Madrid F.;
RT "Molecular cloning, expression, and chromosomal localization of the
RT human earliest lymphocyte activation antigen AIM/CD69, a new member
RT of the C-type animal lectin superfamily of signal-transmitting
RT receptors.";
RL J. Exp. Med. 178:537-547(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93341711; PubMed=8100776;
RA Ziegler S.F., Ramsdell F., Hjerrild K.A., Armitage R.J.,
RA Grabstein K.H., Hennen K.B., Farrah T., Fanslow W.C., Shevach E.M.,
RA Alderson M.R.;
RT "Molecular characterization of the early activation antigen CD69: a
RT type II membrane glycoprotein related to a family of natural killer
RT cell activation antigens.";
RL Eur. J. Immunol. 23:1643-1648(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94298875; PubMed=8026529;
RA Santis A., Lopez-Cabrera M., Hamann J., Strauss M., Sanchez-Madrid F.;
RT "Structure of the gene coding for the human early lymphocyte
RT activation antigen CD69: a C-type lectin receptor evolutionarily
RT related with the gene families of natural killer cell-specific
RT receptors.";
RL Eur. J. Immunol. 24:1692-1697(1994).
CC -1- FUNCTION: INVOLVED IN LYMPHOCYTE PROLIFERATION AND FUNCTIONS AS A
CC SIGNAL TRANSMITTING RECEPTOR IN LYMPHOCYTES, NATURAL KILLER (NK)
CC CELLS, AND PLATELETS.
CC -1- SUBUNIT: HOMODIMER. DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T CELLS,
CC B-CELLS, NATURAL KILLER CELLS, NEUTROPHILS, EOSINOPHILS, EPIDERMAL
CC LANGERHANS CELLS AND PLATELETS.
CC -1- DEVELOPMENTAL STAGE: EARLIEST INDUCIBLE CELL SURFACE GLYCOPROTEIN
CC ACQUIRED DURING LYMPHOID ACTIVATION.
CC -1- INDUCTION: BY ANTIGENS, MITOGENS OR ACTIVATORS OF PKC ON THE
CC SURFACE OF T AND B LYMPHOCYTES. BY INTERACTION OF IL-2 WITH THE
CC P75 IL-2R ON THE SURFACE OF NK CELLS.
CC -1- PTM: CONSTITUTIVE SER/THR PHOSPHORYLATION IN BOTH MATURE
CC THYMOCYTES AND ACTIVATED T LYMPHOCYTES.
CC -1- DATABASE: NAME=PRO; NOTE=CD guide CD69 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd69.htm".
CC
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DR EMBL; L07555; AAB46359.1; -.
DR EMBL; Z22576; CAA80298.1; -.
DR EMBL; Z30426; CAA83017.1; -.
DR EMBL; Z30430; CAA83017.1; JOINED.
DR EMBL; Z30427; CAA83017.1; JOINED.
DR EMBL; Z30429; CAA83017.1; JOINED.
DR EMBL; Z30428; CAA83017.1; JOINED.
DR PIR; JH0822; JH0822.
DR MIM; 107273; -.
DR InterPro; IPR001304; lectin_c.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
KW Antigen: B-cell; Glycoprotein; Transmembrane; Lectin; Signal-anchor;
KW Phosphorylation.
FT DOMAIN 1 40 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 41 61 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT
FT DOMAIN 62 199 (POTENTIAL).
FT DOMAIN 67 199 EXTRACELLULAR (POTENTIAL).
FT DISULFID 68 85 C-TYPE LECTIN (LONG FORM).
FT DISULFID 96 194 BY SIMILARITY.
FT DISULFID 173 186 BY SIMILARITY.
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 199 AA; 22559 MM; 172E269D2FB8DFB CRC64;

Query Match 11.7%; Score 154.5; DB 1; Length 199;
Best Local Similarity 27.6%; Pred. No. 0.00097;
Matches 37; Conservative 18; Mismatches 60; Indels 19; Gaps 6;

OY 115 FSGP-----CPDMLMHNKENCYLFHG-PFGMEKNROTQSILGGQLQINGADDLTFIL 166
DB 74 FSPMPSDHSVSSCEPMVGYQKCYFISTYKRSTSAQNAACSEHGATLAVIDSEKDMNFK 133
OY 167 QAISHTTSPFWIGLHRRKPGQPMIMENGTPLNFOFFKTRGVSLQLYSSNCAYLQDGAYF 226
DB 134 RYAGR-EEHWGL-KKEPGHPMKWSNGKEFN-NMENVLTG-----SDKCYELKNTVEYS 182
OY 227 AENCILIAFSTCOK 240
DB 183 SMECEKNLYWICK 196

Search completed: August 19, 2002, 23:06:57
Job time: 528 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 19, 2002, 22:57:24 ; Search time 68.99 Seconds
(without alignments)
619.361 Million cell updates/sec

Title: US-09-898-554-14
Perfect score: 1319
Sequence: 1 MFEDDKMKRPNDEPDQKSCG.....ENCILIAFISICQKTNHLQI 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriap:*
17: SP archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1241	94.1	363	11 09EQ09	09EQ09 mus musculus
2	972	73.7	364	11 070156	070156 ratius norv
3	643	48.7	278	6 09XTA8	09XTA8 oryctolagus
4	639	48.4	274	6 09TTK7	09TTK7 sus scrofa
5	637	48.3	273	4 P78380	P78380 homo sapien
6	596	45.2	270	6 P79391	P79391 bos taurus
7	258	19.6	247	4 09BXN2	09BXN2 homo sapien
8	251.5	19.1	168	4 096PA7	096PA7 homo sapien
9	251	19.0	201	4 09H1K3	09H1K3 homo sapien
10	231	17.5	244	11 09J150	09J150 mus musculus
11	224.5	17.0	381	6 09SLA8	09SLA8 macaca mula
12	223.5	16.9	381	6 09SLC6	09SLC6 macaca neme
13	223	16.9	360	4 096Q04	096Q04 homo sapien
14	223	16.9	380	4 096Q05	096Q05 homo sapien
15	223	16.9	380	4 096Q00	096Q00 homo sapien
16	223	16.9	404	4 09NNX6	09NNX6 homo sapien

17	223	16.9	404	4 096Q01	096Q01 homo sapien
18	222.5	16.9	404	6 095J96	095J96 macaca mula
19	221	16.8	280	4 09NZH3	09NZH3 homo sapien
20	219.5	16.6	223	11 092563	092563 mus musculus
21	218.5	16.6	217	11 064228	064228 mus sp. nki
22	216.5	16.4	275	11 09D403	09D403 mus musculus
23	212	16.1	268	4 096Q03	096Q03 homo sapien
24	212	16.1	404	6 095198	095198 pan troglod
25	211	16.0	334	4 096Q09	096Q09 homo sapien
26	210	15.9	398	4 096Q08	096Q08 homo sapien
27	206.5	15.7	227	11 092564	092564 mus musculus
28	205	15.5	312	4 096Q07	096Q07 homo sapien
29	204.5	15.5	223	11 099JB4	099JB4 mus musculus
30	204.5	15.5	223	11 099P32	099P32 mus musculus
31	203.5	15.4	295	11 0912M4	0912M4 mus musculus
32	203.5	15.4	311	11 09DBV4	09DBV4 mus musculus
33	203.5	15.4	325	11 091XZ0	091XZ0 mus musculus
34	202.5	15.4	227	11 091V25	091V25 mus musculus
35	201.5	15.3	227	11 091V25	091V25 mus musculus
36	200.5	15.2	223	11 092565	092565 mus musculus
37	195.5	14.8	224	11 061970	061970 mus musculus
38	192.5	14.6	189	11 061969	061969 mus musculus
39	192.5	14.6	263	4 096QP3	096QP3 homo sapien
40	191.5	14.5	229	11 09JL99	09JL99 mus musculus
41	191	14.5	332	4 096QP5	096QP5 homo sapien
42	190	14.4	309	11 063097	063097 ratius norv
43	189.5	14.4	198	11 09DBL1	09DBL1 mus musculus
44	187.5	14.2	156	13 073894	073894 gallus gall
45	186.5	14.1	230	11 054871	054871 ratius norv

ALIGNMENTS

RESULT 1
ID 09EQ09 PRELIMINARY; PRT; 363 AA.
AC 09EQ09;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE OXIDIZED LDL RECEPTOR.
OS LOX-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Park S.-H., Ahn H.-J., Cho J.-J.;
RT "Mouse LOX-1 is expressed in mast cells after Ige cross-linking.";
RL Submitted (SEP-2000) to the EMBL/Genbank/DBD databases.
DR EMBL; AF305744; AAC4498.1; -;
DR InterPro; IPR001304; lectin_c.
DR Pfam; PF000059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_Type_Lectin_2; 1.
KW Receptor.
SQ SEQUENCE 363 AA; 41613 MW; E44703D6408F15F8 CRC64;

Query Match 94.1%; Score 1241; DB 11; Length 363;
Best Local Similarity 67.5%; Pred. No. 4,6e+80;
Matches 245; Conservative 0; Mismatches 2; Indels 116; Gaps 1;
QY 1 MFEDDKMKRPNDEPDQKSCGKRPK----- 24
DB 1 MFEDDKMKRPNDEPDQKSCGKRGHLILSPWMPFAAMTIVILCLVSLTVLIVQNTQLR 60
QY 25 ----- 24
DB 61 QVSDLLKQVAMLTQDRIILEGOMLAQKRAENASQESKRELKIDITLTKINKESKEOE 120

QY 25 -----ESORELKGKIDITLTKLNEKSKROEELLOKNONOALORANSSGPCPDWL 64
DB 121 ELLOKNONOALORANSSORELKGKIDITLTKLNEKSKROEELLOKNONOALORANSSGPCPDWL 180
QY 65 RAANSSSEORELKGKIDITLTKLNEKSKROEELLOKNONOALORANSSGPCPDWL 124
DB 181 RAANSSSEORELKGKIDITLTKLNEKSKROEELLOKNONOALORANSSGPCPDWL 240
QY 125 WHKENCYLFHGFPGEMENKROTCOSLQGLQINGADDLFTLQAISHTSPFWIGLHRK 184
DB 241 WHKENCYLFHGFPGEMENKROTCOSLQGLQINGADDLFTLQAISHTSPFWIGLHRK 300
QY 185 PGQPLWENGTPPLNFOPFKTRGVSLQLYSSNCAYLQDGAFAENCILIAFSICOKKTNH 244
DB 301 PGQPLWENGTPPLNFOPFKTRGVSLQLYSSNCAYLQDGAFAENCILIAFSICOKKTNH 360
QY 245 LQI 247
DB 361 LQI 363

RESULT 2

ID 070156 PRELIMINARY: PRT: 364 AA.

AC 070156;
DT 01-AUG-1998 (TREMUREL. 07, Created)
DT 01-AUG-1998 (TREMUREL. 07, Last sequence update)
DT 01-JUN-2001 (TREMUREL. 17, Last annotation update)
DE ENDOTHELIAL RECEPTOR FOR OXIDIZED LOW-DENSITY LIPOPROTEIN.
GN LOX-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SHR-SP; TISSUE-KIDNEY.
RA MEDLINE=98161826; PubMed=9494115;
RA Nagase M., Hirose S., Fujita T.;
RT "Unique repetitive sequence and unexpected regulation of expression of rat endothelial receptor for oxidized low-density lipoprotein (LOX-1)."
RT Blochem. J. 330:1417-1422(1998).
RL [2]
RN SEQUENCE FROM N.A.
RP STRAIN-SERAGUE-DAWLEY; TISSUE-LIVER;
RC MEDLINE=99057940; PubMed=9837956;
RA Nagase M., Abe J., Takahashi K., Ando J., Hirose S., Fujita T.;
RT "Genomic organization and regulation of expression of the lectin-like oxidized low-density lipoprotein receptor (LOX-1) gene."
RT J. Biol. Chem. 273:33702-33707(1998).
RL EMBL; AB005900; BAA25785.1; -;
DR EMBL; AB018104; BAA35123.1; JOINED.
DR EMBL; AB018097; BAA35123.1; JOINED.
DR EMBL; AB018098; BAA35123.1; JOINED.
DR EMBL; AB018099; BAA35123.1; JOINED.
DR EMBL; AB018100; BAA35123.1; JOINED.
DR EMBL; AB018101; BAA35123.1; JOINED.
DR EMBL; AB018102; BAA35123.1; JOINED.
DR EMBL; AB018103; BAA35123.1; JOINED.
DR Interpro: IPR001304; lectin_c.
DR Pfam: PF000059; lectin_c; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
KW Lipoprotein; Receptor; Lectin.
SQ SEQUENCE 364 AA; 41890 MW; 0AD2839C07206E09 CRC64;

Query Match 73.7%; Score 972; DB 11; Length 364;
Best Local Similarity 53.2%; Pred. No. 4.3e-61;
Matches 192; Conservative 22; Mismatches 30; Indels 116; Gaps 2;

24

DB 1 MAFDKMKPVNGOPDOKSCGKPKGLHLSSSTMCPAAVTLAILCLVSLTVQOTQL 60
QY 25 -----ESORELKGKIDITLTKLNEKSKROEELLOKNONOALORANSSGPCPDWL 50
DB 61 QVSDLLKQYANLTQODHILEGOMSAOKKAMASOESRELKEIDITLTKLNEKSKROE 120
QY 51 ELLOKNONOALORANSS-----69
DB 121 KLLOKNONOALORAVANSEESKWELEKQIDILNMKLNISKROKELLQONONALQALQ 180
QY 70 -----SESORELKGKIDITLTKLNEKSKROEELLOKNONOALORANSSGPCPDWL 124
DB 181 KAERYSESORELKEQIDITLSWKLNKSKROEELLOKNONOALORANSSGPCPDWL 240
QY 125 WHKENCYLFHGFPGEMENKROTCOSLQGLQINGADDLFTLQAISHTSPFWIGLHRK 184
DB 241 WHKENCYLFHGFPGEMENKREKSLDQLOISTDNLFTLQATSHSTSPFWIGLHRK 300
QY 185 PGQPLWENGTPPLNFOPFKTRGVSLQLYSSNCAYLQDGAFAENCILIAFSICOKKTNH 244
DB 301 PNHPLWENGSPLSFOPFKTRGVSLQWYSSGTCAYIQQGVFAENCILIAFSICOKKANL 360
QY 245 L 245
DB 361 L 361

RESULT 3

ID 09XTA8 PRELIMINARY: PRT: 278 AA.

AC 09XTA8;
DT 01-NOV-1999 (TREMUREL. 12, Created)
DT 01-NOV-1999 (TREMUREL. 12, Last sequence update)
DT 01-DEC-2001 (TREMUREL. 19, Last annotation update)
DE LECTIN-LIKE OXIDIZED LDL RECEPTOR.
GN LOX-1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Sawamura T., Chen M.;
RT "Rabbit lectin-like oxidized LDL receptor 1."
RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016237; BAA81912.1; -;
DR Interpro: IPR001304; lectin_c.
DR Pfam: PF000059; lectin_c; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 278 AA; 31646 MW; 25A5E310F823A09B CRC64;

Query Match 48.7%; Score 643; DB 6; Length 278;
Best Local Similarity 49.3%; Pred. No. 5.1e-38;
Matches 135; Conservative 39; Mismatches 70; Indels 30; Gaps 6;

QY 1 MTFPD-KKKPANDPDKSCGKPKRESOREL-----GKIDITR---40
DB 5 MAVDDLKVPKPKDOPDOKSNGKPKR--GLRFLSSPMWCPAAVVALGVLCLGSLMTITIMGM 62
QY 41 ---RLDEKSKROEELLOKNONOALORANSSSEORELKGKIDITLTKLNEKSK 93
DB 63 QILOVSDLLKQOQANLTQODHILEGOMSAOKKAMASOESRELKEIMETLAKRLDEKSK 122
QY 94 EOELLQKNONOALORANSSGPCPDWLWHKENCYLF-HGPGEMENKROTCOSLQGLQ 152
DB 123 KOMELNHQYLNLOALALKRMDFSGPCPDWLHMGKNCYLIFSSGFFWNESSOKEKCLSDAQ 182
QY 153 LLOINGADDLFTLQAISHTSPFWIGLHRKPKQPLWENGTPPLNFOPFKTRGVSLQLY 212

ID	Q9TTK7	PRELIMINARY:	PRT:	274 AA.
AC	01-MAY-2000 (TREMBlrel. 13, Created)			
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)			
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)			
DE	LECTIN-LIKE OXIDIZED LDL RECEPTOR-1.			
GN	PLOX-1.			
OS	Sus scrofa (pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
NCBI	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
NCBI	_taxid=9823;			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=21181560; PubMed=11284714;			
RT	Chen M., Natumiya S., Masaki T., Sawamura T.;			
RT	"Conserved C-terminal residues within the lectin-like domain of LOX-1			
RT	are essential for oxidized low-density-lipoprotein binding.";			
RL	Biochem. J. 355:289-296(2001).			
DR	EMBL: AB018668; BAA88894.1; -			
DR	InterPro: IPR001304; Lectin_c.			
DR	Pfam: PF00059; Lectin_c.1.			
DR	SMART: SM00034; CLECT; 1.			
DR	PROSITE: PS50041; C_Type_Lectin_2; 1.			
DR	RECEPTOR.			
DR	SEQUENCE 274 AA; 31142 MW; D141776C79FB42E0 CRC64;			
QY	1 MTFDD-KMKPADEPDOKSGCKRPPEESORELK-----			
DB	1 MTLDDKSNMSMDQDEDSNG--DKAEGRSLSTLRMRPALILGLICGLVTVLLII 58			
QY	33 --GKIDITTRKLDEKSKDEDELLQMIQNLQALQRAANSSEDSORELKGIDITLTKLNE 90			
DB	59 QLSQSDILKQKVKLTTHQEDIL---EGALQROAKESQSSQRELTRETLAHLKIDE 115			
QY	91 KSKDEELLQKNQNLQALQRAANSNGPCPDWLMEHCKCYFSSQPFSEKSSRENCISL 149			
DB	116 KSKLMEILOQQLNLQALQRAANSNGPCPDWLMEHCKCYFSSQPFSEKSSRENCISL 175			
QY	150 GGQLIQINGADDLFTLLQAIHSHTSPFWIGLHRRKPGQWMLWNGTPLNFOFFKTRGVS 209			
DB	176 DAQLIKINSTDLDEFIQQIHAHSPFWMGSLSRKNSNMLWLEDGTPPLPHLFRLOGAAS 235			
QY	210 QLYSSNCAYLQDGAFAFNCILIAFSTQCKTKNHQ 246			
DB	236 QMYPSGTCAVYHKGIVFAFNCILIAFSTQCKTKANLRL 272			
RESULT	5			
ID	P78380			
AC	P78380.			
DT	01-MAY-1997 (TREMBlrel. 03, Created)			
DT	01-MAY-1997 (TREMBlrel. 03, Last sequence update)			
DT	01-JUN-2001 (TREMBlrel. 17, Last annotation update)			
DE	LECTIN-LIKE OXIDIZED LDL RECEPTOR.			
GN	LOX-1 OR OLRL.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			

OX	NCHI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=LUNG;
RX	MEDLINE=97205278; PubMed=9052782;
RA	Sawamura T., Kune N., Aoyama T., Moriwaki H., Hoshikawa H., Alba Y.,
RA	Tanaka T., Miwa S., Katsura Y., Kita T., Masaki T. ;
RT	"An endothelial receptor for oxidized low-density lipoprotein.";
RL	Nature 386:73-77(1997).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=BLOOD;
RA	Millar D.S.;
RL	Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A.
RA	Li X., Bouzyk M.M., Wang X.K.;
RT	"Human oxidized low density lipoprotein receptor: characterization of
RT	the full length cDNA sequence and assignment to human chromosome
RT	12p13.1-12.3."
RL	Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
RN	[4]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=99047525; PubMed=9828121;
RA	Yamanaka S., Zhang X.Y., Miura K., Kim S., Iwao H.;
RA	"The human gene encoding the lectin-type oxidized LDL receptor (OLR1)
RT	is a novel member of the natural killer gene complex with a unique
RT	expression profile."
RL	Genomics 54:191-199(1998).
DR	EMBL, AB010710; BAA24380.1; -
DR	EMBL, AJ131757; CAB38175.1; -
DR	EMBL, AF035776; AAC8329.1; -
DR	EMBL, AF079167; AAC97927.1; -
DR	EMBL, AF079164; AAC97927.1; JOINED.
DR	EMBL, AF079165; AAC97927.1; JOINED.
DR	EMBL, AF079166; AAC97927.1; JOINED.
DR	InterPro: IPR01304; Lectin_c.
DR	Pfam: PF00059; lectin_c; 1.
DR	SMART: SM0034; CLECT; 1.
DR	PROSITE: PS0041; C.TYPE.LECTIN_2; 1.
KW	Lectin; Receptor; Lipoprotein.
SO	SEQUENCE 273 AA; 30959 MW; 852DE659DCD3D361 CRC64;

DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE LECTIN-LIKE OXIDIZED LDL RECEPTOR.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 ON NCBI_TaxId=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97205278; PubMed=9052782;
 RA Sawamura T., Kume N., Aoyama T., Moriaki H., Hoshikawa H., Aiba Y.,
 RA Tanaka T., Miwa S., Katsura Y., Kita T., Masaki T.;
 RT "An endothelial receptor for oxidized low-density lipoprotein.";
 RL Nature 386:73-77(1997).
 DR EMBL: D89049; BAA19005.1; -
 DR HSSP: P20693; 1HLJ.
 DR InterPro: IPR001304; lectin_c.
 DR Pfam: PF00059; lectin_c; 1.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
 KW Receptor.
 SQ SEQUENCE: 270 AA; 30892 MW; 6055B681AD7053D CRC64;

Query Match 45.2%; Score 596; DB 6; Length 270;
 Best Local Similarity 44.6%; Pred. No. 1e-34;
 Matches 125; Conservative 39; Mismatches 70; Indels 46; Gaps 6;

QY 1 MTDDMKRPNDEPKSCGKRPK-----ESSQR 29
 DB 1 MTVDPP-KGKKDDLDQKPNKTAKEVSWRWYPAATLVGLGLVTVILLILQLSQ- 58
 QY 30 ELKGKIDITRKADSKSEKQELL--OMIQNLQALQRAANSSESEORELKGKIDITLTK 87
 DB 59 -----VSDLRKKQOANTTHQEDILEGOIL-----AQRSEKSAQESQELKEMLETIAHK 108
 QY 88 LNKESKEQELLQKQNLQALQRAANSFGPCPDMLMKENCYLF-HGPFGEKKNROT 146
 DB 109 LDRKSKMLKHLRQNLQALQRAANSFGPCPDMLMKENCYLF-HGPFGEKKNROT 168
 QY 147 QSIAGGQLQINGADDLFTLILQAISSHTTSPFWIGLHKKKPGQPMWENGTPLPNPFSTRG 206
 DB 169 LSLDAHLKLTNSDELEFIQOMIAHSSFPWMLGSLMKPYSWLMWEDGTPLPNPFSTRG 228
 QY 207 VSIQVSLQYSSNCAYLQDGAFAENCILIAFSICOKKTNHLO 246
 DB 229 AVSRMYPSCGICATYQKGTVAENCILIAFSICOKKANLKR 268

RESULT 7
 Q9BXN2 PRELIMINARY; PRT; 247 AA.
 AC 09BXN2; 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE DENDRITIC CELL-ASSOCIATED C-TYPE LECTIN-1 (DECTIN-1 RECEPTOR)
 DE (LECTIN-LIKE RECEPTOR 1) (BETA-GLUCAN RECEPTOR ISOFORM A).
 GN DECTIN-1 OR DECTIN1 OR BGR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 ON NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21363425; PubMed=11470510;
 RA Yokota K., Takashima A., Bergstresser P.R., Arizumi K.;
 RT "Identification of a human homologue of the dendritic cell-associated
 RT C-type lectin-1, dectin-1.";
 RL Gene 272:51-60(2001).
 RN [2]

RP SEQUENCE FROM N.A.
 RA Sobhanov Y., Bernreiter A., Derdak S., Mechtcheriakova D., Duechler M.,
 RA Kalhoff F., Hofer E.;
 RT "A novel cluster of lectin-like receptor genes expressed in monocytic,
 RT dendritic and endothelial cells maps close to the NK receptor genes in
 RT the human NK gene complex.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21383615; PubMed=11491532;
 RA Hernandez-Falcon P., Arce I., Roda-Navarro P., Fernandez-Ruiz E.;
 RT "Cloning of human DECTIN-1, a novel C-type lectin-like receptor gene
 RT expressed on dendritic cells.";
 RL Immunogenetics 53:288-295(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Herranz-Falcon P., Arce I., Fernandez-Ruiz E.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PERIPHERAL BLOOD LEUKOCYTE;
 RA Willment J.A., Gordon S., Brown G.D.;
 RT "Characterization of the human beta-glucan receptor and its
 RT alternatively spliced isoforms.";
 RL J. Biol. Chem. 0:0-0(2001).
 DR EMBL: AF313468; AAK37473.1; -
 DR EMBL: AF312373; CAC43847.1; -
 DR EMBL: AY026769; AAK20114.2; -
 DR EMBL: AF400595; AAL11711.1; -
 DR InterPro: IPR002353; Antifreezeit.
 DR Pfam: PF00059; lectin_c; 1.
 DR PRINTS: PR00356; ANTIFREEZEIT.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
 KW Lectin; Receptor.
 SQ SEQUENCE: 247 AA; 27627 MW; 98393E36976111B9 CRC64;

Query Match 19.6%; Score 258; DB 4; Length 247;
 Best Local Similarity 31.2%; Pred. No. 6.3e-11;
 Matches 50; Conservative 41; Mismatches 65; Indels 4; Gaps 3;

QY 86 LKLNKSKQ--EELLQKQNLQALQRAANSFGPCPDMLMKENCYLFHGPFGEKKNROT 142
 DB 85 LSRKKNHSGPTQSSLDSTYPTKAVKTGVLSSPCPNMITYEKSCYLSMSLNSWDGS 144
 QY 143 RQTCQSIAGGQLQINGADDLFTLILQAISSHTTSPFWIGLHKKKPGQPMWENGTPLPNPFSTRG 201
 DB 145 KRQCMQGLGSLNKLKIDSSNELGEFIVKQVSSQPDNSFWIGLSPQTEVPMWEDGSTFSSNL 204
 QY 202 FKTRVSLQYSSNCAYLQDGAFAENCILIAFSICOKK 241
 DB 205 FQIRTTATQENPSPNCVWYHVSYYIDQLCSVPSISICEK 244

RESULT 8
 Q96PA7 PRELIMINARY; PRT; 168 AA.
 AC 096PA7; 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
 DE BETA-GLUCAN RECEPTOR ISOFORM E.
 GN BGR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 ON NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Willment J.A., Gordon S., Brown G.D.;
 RT "Characterization of the human beta-glucan receptor and its

RT alternatively spliced isoforms."
 RL J. Biol. Chem. 0:0(2001).
 DR EMBL: AF400599; AAL11715.1; -
 KW Receptor.
 SQ SEQUENCE 168 AA; 19217 MW; AFD3A8F89BBFFC6 CRC64;

Query Match 19.1%; Score 251.5; DB 4; Length 168;
 Best Local Similarity 32.6%; Pred. No. 1.2e-10;
 Matches 47; Conservative 35; Mismatches 59; Indels 3; Gaps 3;

QY 100 QKNOIAGALORANFSGPCPDWLMHKENCYLFGPFGF-GWEKNROTCSLGGOLQJNG 158
 DB 23 QSNTRIAVAVSEKV-LSSPCPPNWIYERKCYLFMSLSNWDGSKRQCGQLGSLNLIKIDS 81
 QY 159 ADDLFLIL-QAISHTSFPGWGLHKKKQGPWLMENGTPNLNQFKTRGVSLQLYSSSNC 217
 DB 82 SNELEFIVKQVSSQDPNSFVIGLSRPQTEVPWLMEDGSTFSSNLFOIRTTAQENPSPNC 141
 QY 218 AYLQDAVFAENCILAFSICOKK 241
 DB 142 VWIHVSIVYDOLCSVPSYSICEKK 165

RESULT 9
 Q9H1K3 PRELIMINARY; PRT; 201 AA.
 ID Q9H1K3
 AC Q9H1K3;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PUTATIVE TRANSMEMBRANE PROTEIN DECTIN-1 (DENDRITIC CELL-ASSOCIATED C-
 DE TYPE LECTIN-1 BETA) (DECTIN-1 RECEPTOR) (LECTIN-LIKE RECEPTOR 1B)
 DE (BETA-GLUCAN RECEPTOR ISOPFORM B).
 GN DECTIN-1 OR DECTINI OR BGR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Grunebach F., Brugger W., Kanz L., Brossart P.;
 RT "Identification of the human dendritic-cell-associated molecule,
 RT hdectin-1, by cDNA subtraction and Rapid Amplification of cDNA Ends
 RT (RACE).";
 RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yokota K., Takashima A., Bergstresser P.R., Arizumi K.;
 RT "Identification of a Human Homolog of the Dendritic Cell-associated C-
 RT type lectin-1, Dectin-1.";
 RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Sobanov V., Bernstetter A., Derdak S., Mechtcheriakova D., Duechler M.,
 RA Kalthoff F., Hofer E.;
 RT "A novel cluster of lectin-like receptor genes expressed in monocytic,
 RT dendritic and endothelial cells maps close to the NK receptor genes in
 RT the human NK gene complex.";
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21383615; PubMed=11491532;
 RA Hernandez-Falcon P., Arce I., Roda-Navarro P., Fernandez-Ruiz E.;
 RT "Cloning of human DECTIN-1, a novel C-type lectin-like receptor gene
 RT expressed on dendritic cells.";
 RL Immunogenetics 53:288-295(2001).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Hernandez-Falcon P., Arce I., Fernandez-Ruiz E.;
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.

RC TISSUE=PERIPHERAL BLOOD LEUKOCYTE;
 RA Willment J.A., Gordon S., Brown G.D.;
 RT "Characterization of the human beta-glucan receptor and its
 RT alternatively spliced isoforms.";
 RL J. Biol. Chem. 0:0(2001).
 DR EMBL: AY009090; AAG35923.2; -
 DR EMBL: AF313469; AAK37474.1; -
 DR EMBL: AJ312372; CAC43846.1; -
 DR EMBL: AY026770; AAK20115.1; -
 DR EMBL: AF400596; AAL11712.1; -
 DR InterPro: IPR002353; Antifreeze1.
 DR InterPro: IPR001304; lectin_c.
 DR Pfam: PF00059; lectin_c; 1.
 DR PRINTS: PR00356; ANTIFREEZE1.
 DR SMART: SM00034; CLECT. 1.
 DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
 KW Transmembrane; Lectin; Receptor.
 SQ SEQUENCE 201 AA; 22563 MW; C6ADEE762B2CE968 CRC64;

Query Match 19.0%; Score 251; DB 4; Length 201;
 Best Local Similarity 35.2%; Pred. No. 1.6e-10;
 Matches 45; Conservative 32; Mismatches 49; Indels 2; Gaps 2;

QY 116 SGPCPDWLMHKENCYLFGPFGF-GWEKNROTCSLGGOLQJNGADLFTIL-QAISHPT 173
 DB 71 SSSPCPPNWIYERKCYLFMSLSNWDGSKRQCGQLGSLNLELEFIVKQVSSQDP 130
 QY 174 SPFWGLHKKKQGPWLMENGTPNLNQFKTRGVSLQLYSSSNCAYLQDAVFAENCIL 233
 DB 131 NSWGLSLRPQTEVPWLMEDGSTFSSNLFOIRTTAQENPSPNCVWIVHSIVYDOLCSVP 190
 QY 234 AFSICOKK 241
 DB 191 SYSICEKK 198

RESULT 10
 Q9J150 PRELIMINARY; PRT; 244 AA.
 ID Q9J150
 AC Q9J150;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE DENDRITIC CELL-ASSOCIATED C-TYPE LECTIN-1.
 GN CLECSF12 OR DECTIN-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=20347934; PubMed=10779524;
 RA Arizumi K., Shen G.-L., Shikano S., Xu S., Rittner R. III,
 RA Kumamoto T., Edelbaum D., Morita A., Bergstresser P.R., Takashima A.;
 RT "Identification of a novel, dendritic cell-associated molecule,
 RT dectin-1, by subtractive cDNA cloning.";
 RL J. Biol. Chem. 275:20157-20167(2000).
 DR EMBL: AF262985; AAF72710.1; -
 DR MGI: 1861431; Clecsf12.
 DR InterPro: IPR001304; lectin_c.
 DR Pfam: PF00059; lectin_c; 1.
 DR SMART: SM00034; CLECT. 1.
 DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
 KW Lectin.
 SQ SEQUENCE 244 AA; 27621 MW; 55A71C04E68CA002 CRC64;

Query Match 17.5%; Score 231; DB 11; Length 244;
 Best Local Similarity 30.9%; Pred. No. 5e-09;
 Matches 50; Conservative 27; Mismatches 83; Indels 2; Gaps 2;

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OY 82 DTTLTLNLSKSKQOEELLQNNQLOALQRAANFSGPCPODWLMHKNCTYLF-HGPGWE 140
DB 82 DNLSRKNKHNKPTSSLDKVAAPSKQTTPGOSCLPNWIMHKGSCYLFSGSGMSWY 141
OY 141 KNOTOOSLGGLLOINGADLTFI-LQAISSHTPSPWILHKKRPOPLMENGFTLNF 199
DB 142 GSRHKSQDLAHLTKIDNSKEPFESQTSRHINAFWIGSRKOSGCPWFMEGSAFP 201
OY 200 QEFKTRGVSLQYSSNCAYLQDGAFAENCILIAFSICOK 241
DB 202 NSFQVNTVPQESLHNCVMIHSEVYNQICNNSSYSICEKE 243

RESULT 11
O95L8 PRELIMINARY; PRT; 381 AA.
ID O95L8;
AC O95L8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE DENDRITIC CELL-SPECIFIC ICAM-3 GRABBING NONINTEGRIN.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
NCBI_TaxID=9544;
RN [1]
RX MEDLINE=21465051; PubMed=11581396;
RA Barilaud F., Pohlmann S., Sparwasser T., Kimata M.T., Choi Y.K.,
RA Haggerty B.S., Ahmad N., Macfarlan T., Edwards T.G., Leslie G.J.,
RA Arnason J., Reinhart T.A., Kimata J.T., Littman D.R., Hoxie J.A.,
RA Doms R.W.;
RT "Functional and antigenic characterization of human, rhesus macaque,
RT pigtailed macaque, and murine dc-sign.";
RL J. Virol. 75:10281-10289(2001).
DR EMBL: AF369755; AAL14438.1; -.
KW Integrin.
SQ SEQUENCE 381 AA; 42897 MW; 01FE7B0B42C91D49 CRC64;

Query Match 17.0%; Score 224.5; DB 6; Length 381;
Best Local Similarity 25.8%; Pred. No. 2.3e-08;
Matches 74; Conservative 50; Mismatches 98; Indels 65; Gaps 13;

OY 6 KMRPANDPPOKS-----CGKRPRESOREL-----KGK 34
DB 83 QLKVAVSELSKSKQOEIYQELTRLKAAGVGLPEKSKQOEIYQELTRLKAAGVGLPEKSK 142
OY 35 IDTI-----TR-----KLDEKSKQOEELQNNQLOALQRAANFSGPCPODWLMHKNCTYLF 79
DB 143 LQEIYQELTRLKAAGVGLPEKSK-QOEIYQELTRLKAAGVGLPEKSKQOEIYQELTRLKA 201
OY 80 KIDTLTLKLNKSKQOE---ELLQNNQLOALQRAANFSGPCPODWLMHKNCTYLFHG 135
DB 202 AVGLP-----DRSKQOEIYQELI-----LKAVERLCR---PCWEMTFPGNCTYFMSNS 250
OY 136 PFGMEKNRQTCQSLGGOLLOINGADLTFILQAISSHTPSPWILHKKRPOPLMENGFT 195
DB 251 QRNMHNSITACQEVGADLVYKSAEQNFLOLQSSRSNRFWMGLSLDNLHGTQWVDGS 310
OY 196 PL--NPOEFKTRGVSLQYSSNCAYLQDGAFAENCILIAFSICOK 240
DB 311 PLPSPFQYWNKGPNNV-GEEDCAEFGSGNGMDDCKNLAKFWICK 356

RESULT 12
O95LC6 PRELIMINARY; PRT; 381 AA.
ID O95LC6;
AC O95LC6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
SQ SEQUENCE 360 AA; 41009 MW; 6ABE2B9AAEDFAA8 CRC64;

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DE DENDRITIC CELL-SPECIFIC ICAM-3 GRABBING NONINTEGRIN.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
NCBI_TaxID=9545;
RN [1]
RX MEDLINE=21465051; PubMed=11581396;
RA Barilaud F., Pohlmann S., Sparwasser T., Kimata M.T., Choi Y.K.,
RA Haggerty B.S., Ahmad N., Macfarlan T., Edwards T.G., Leslie G.J.,
RA Arnason J., Reinhart T.A., Kimata J.T., Littman D.R., Hoxie J.A.,
RA Doms R.W.;
RT "Functional and antigenic characterization of human, rhesus macaque,
RT pigtailed macaque, and murine dc-sign.";
RL J. Virol. 75:10281-10289(2001).
DR EMBL: AF343727; AAL14428.1; -.
KW Integrin.
SQ SEQUENCE 381 AA; 42951 MW; C4F6E23D454B74A CRC64;

Query Match 16.9%; Score 223.5; DB 6; Length 381;
Best Local Similarity 25.8%; Pred. No. 2.7e-08;
Matches 74; Conservative 51; Mismatches 97; Indels 65; Gaps 13;

OY 6 KMRPANDPPOKS-----CGKRPRESOREL-----KGK 34
DB 83 QLKVAVSELSKSKQOEIYQELTRLKAAGVGLPEKSKQOEIYQELTRLKAAGVGLPEKSK 142
OY 35 IDTI-----TR-----KLDEKSKQOEELQNNQLOALQRAANFSGPCPODWLMHKNCTYLF 79
DB 143 LQEIYQELTRLKAAGVGLPEKSK-QOEIYQELTRLKAAGVGLPEKSKQOEIYQELTRLKA 201
OY 80 KIDTLTLKLNKSKQOE---ELLQNNQLOALQRAANFSGPCPODWLMHKNCTYLFHG 135
DB 202 AVGLP-----DRSKQOEIYQELI-----LKAVERLCR---PCWEMTFPGNCTYFMSNS 250
OY 136 PFGMEKNRQTCQSLGGOLLOINGADLTFILQAISSHTPSPWILHKKRPOPLMENGFT 195
DB 251 QRNMHNSITACQEVGADLVYKSAEQNFLOLQSSRSNRFWMGLSLDNLHGTQWVDGS 310
OY 196 PL--NPOEFKTRGVSLQYSSNCAYLQDGAFAENCILIAFSICOK 240
DB 311 PLPSPFQYWNKGPNNV-GEEDCAEFGSGNGMDDCKNLAKFWICK 356

RESULT 13
O96Q04 PRELIMINARY; PRT; 360 AA.
ID O96Q04;
AC O96Q04;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SPC-SIGNIA TYPE II ISOFORM.
GN CD209.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RX MEDLINE=2137487;
RA Nummudi S., Catano G., Lam L., Hoefle A., Telles V., Begum K.,
RA Jimenez F., Ahuja S.S., Ahuja S.K.;
RT "Extensive repertoire of Membrane-bound and soluble Dendritic Cell-
RT specific ICAM-3-grabbing Nonintegrin 1 (DC-SIGN1) and DC-SIGN2
RT isoforms. Inter-individual Variation In Expression of DC-SIGN
RT transcripts.";
RL J. Biol. Chem. 276:33196-33212(2001).
DR EMBL: AY042226; AAK91851.1; -.
SQ SEQUENCE 360 AA; 41009 MW; 6ABE2B9AAEDFAA8 CRC64;

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Query Match 16.9%; Score 223; DB 4; Length 360;
Best Local Similarity 26.0%; Pred. No. 2.8e-08;
Matches 67; Conservative 54; Mismatches 107; Indels 30; Gaps 10;

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OY 6 KMKPANDPEPOKS-----CGKKPKESORELKGI DTI---TRKIDEKSK 47
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Db 85 RLKAAVGLPEKSKIOEIYQELTWLKAAGVGLPEKSKMOEITRLKAAVGLPEKSK 144
   :| | | | |
OY 48 EOELLQMIQLOALORAANSSESO--RELKGI DTITLTKLNKSKOEELLQKNOML 105
   :| | | | |
Db 145 -QOEIYQELTRKAAVGLPEKSKQOEIYQELT-RLKAAVGLPEKSK-QOEIYQELTQL 201
   :| | | | |
OY 106 QEALORANFSGPCPODWLHKENCY-LFHGPFGEKNRQTCOSLGQLQINGADLTF 164
   :| | | | |
Db 202 KAAVERLCH---PCPWMTFFQNCYFMSNSQRNMHDSITACKEVGAQLVYKSAEQNF 258
   :| | | | |
OY 165 ILQAI SHTTSPWIGLHRRKKGQPLWENGTP--NFOFKTRGVSLQYSSNCAYIAD 222
   :| | | | |
Db 259 LQLOSSRSNRFTWMGLSDINQEGTWQWDGSPLLPFSKOYNNRGPNNV-GEEDCAEFSG 317
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OY 223 GAVFAENCILIAFSICOK 240
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Db 318 NGWMDKCNLAKFWICK 335
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RESULT 14

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096005 PRELIMINARY; PRT; 380 AA.
AC 096005;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SDC-SIGNIA TYPE I ISOFORM.
CN C209.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11337487;
RA Mummidi S., Catano G., Lam L., Hoeffle A., Telles V., Begum K.,
RA Jimenez F., Ahuja S.S., Ahuja S.K.;
RT "Extensive Repertoire of Membrane-bound and Soluble Dendritic Cell-
RT specific ICAM-3-grabbing Nonintegrin 1 (DC-SIGN1) and DC-SIGN2
RT Isoforms. Inter-individual Variation in Expression of DC-SIGN
RT Transcripts.";
RL J. Biol. Chem. 276:33196-33212(2001).
DR EMBL; AY042225; AAK91850.1; -.
SQ SEQUENCE 380 AA; 43330 MW; BCF9CC45ABEF6B02 CRC64;
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Query Match 16.9%; Score 223; DB 4; Length 380;
Best Local Similarity 26.0%; Pred. No. 3e-08;
Matches 67; Conservative 54; Mismatches 107; Indels 30; Gaps 10;

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OY 6 KMKPANDPEPOKS-----CGKKPKESORELKGI DTI---TRKIDEKSK 47
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Db 105 RLKAAVGLPEKSKIOEIYQELTWLKAAGVGLPEKSKMOEITRLKAAVGLPEKSK 164
   :| | | | |
OY 48 EOELLQMIQLOALORAANSSESO--RELKGI DTITLTKLNKSKOEELLQKNOML 105
   :| | | | |
Db 165 -QOEIYQELTRKAAVGLPEKSKQOEIYQELT-RLKAAVGLPEKSK-QOEIYQELTQL 221
   :| | | | |
OY 106 QEALORANFSGPCPODWLHKENCY-LFHGPFGEKNRQTCOSLGQLQINGADLTF 164
   :| | | | |
Db 222 KAAVERLCH---PCPWMTFFQNCYFMSNSQRNMHDSITACKEVGAQLVYKSAEQNF 278
   :| | | | |
OY 165 ILQAI SHTTSPWIGLHRRKKGQPLWENGTP--NFOFKTRGVSLQYSSNCAYIAD 222
   :| | | | |
Db 279 LQLOSSRSNRFTWMGLSDINQEGTWQWDGSPLLPFSKOYNNRGPNNV-GEEDCAEFSG 337
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OY 223 GAVFAENCILIAFSICOK 240
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Db 338 NGWMDKCNLAKFWICK 355

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RESULT 15
096000 PRELIMINARY; PRT; 380 AA.
AC 096000;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SDC-SIGNIB TYPE I ISOFORM.
CN C209.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11337487;
RA Mummidi S., Catano G., Lam L., Hoeffle A., Telles V., Begum K.,
RA Jimenez F., Ahuja S.S., Ahuja S.K.;
RT "Extensive Repertoire of Membrane-bound and Soluble Dendritic Cell-
RT specific ICAM-3-grabbing Nonintegrin 1 (DC-SIGN1) and DC-SIGN2
RT Isoforms. Inter-individual Variation in Expression of DC-SIGN
RT Transcripts.";
RL J. Biol. Chem. 276:33196-33212(2001).
DR EMBL; AY042230; AAK91851.1; -.
SQ SEQUENCE 380 AA; 43125 MW; F3D098F9FB7D044B CRC64;
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Query Match 16.9%; Score 223; DB 4; Length 380;
Best Local Similarity 26.0%; Pred. No. 3e-08;
Matches 67; Conservative 54; Mismatches 107; Indels 30; Gaps 10;

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OY 6 KMKPANDPEPOKS-----CGKKPKESORELKGI DTI---TRKIDEKSK 47
   :| | | | |
Db 105 RLKAAVGLPEKSKIOEIYQELTWLKAAGVGLPEKSKMOEITRLKAAVGLPEKSK 164
   :| | | | |
OY 48 EOELLQMIQLOALORAANSSESO--RELKGI DTITLTKLNKSKOEELLQKNOML 105
   :| | | | |
Db 165 -QOEIYQELTRKAAVGLPEKSKQOEIYQELT-RLKAAVGLPEKSK-QOEIYQELTQL 221
   :| | | | |
OY 106 QEALORANFSGPCPODWLHKENCY-LFHGPFGEKNRQTCOSLGQLQINGADLTF 164
   :| | | | |
Db 222 KAAVERLCH---PCPWMTFFQNCYFMSNSQRNMHDSITACKEVGAQLVYKSAEQNF 278
   :| | | | |
OY 165 ILQAI SHTTSPWIGLHRRKKGQPLWENGTP--NFOFKTRGVSLQYSSNCAYIAD 222
   :| | | | |
Db 279 LQLOSSRSNRFTWMGLSDINQEGTWQWDGSPLLPFSKOYNNRGPNNV-GEEDCAEFSG 337
   :| | | | |
OY 223 GAVFAENCILIAFSICOK 240
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Db 338 NGWMDKCNLAKFWICK 355
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